peptide selection

peptide optimization

formation of Fc-peptide DNA construct

insertion of construct into expression vector

transfection of host cell with vector

expression of vector in host cell

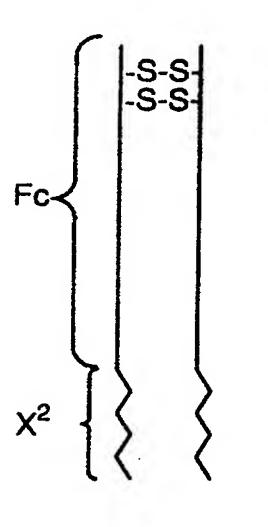
Fc multimer formation in host cell

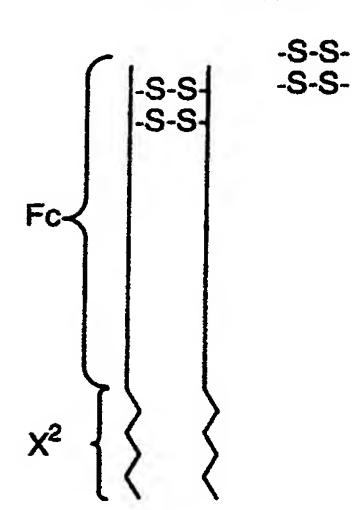
isolation of Fc multimer from host cell

FIG. 2A

FIG. 2B

FIG. 2C





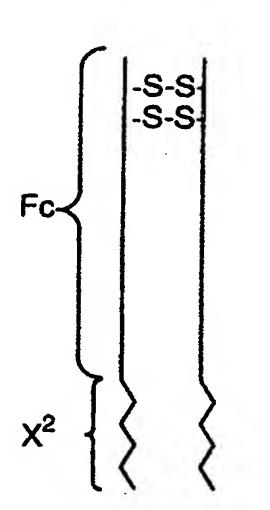
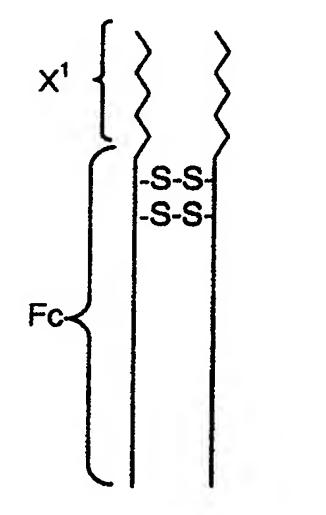
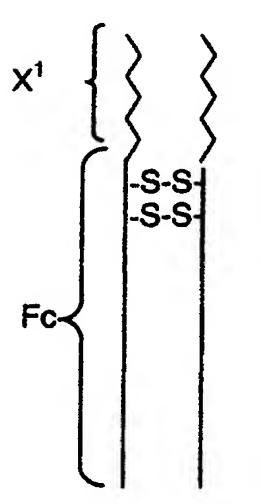


FIG. 2D FIG. 2E

FIG. 2F





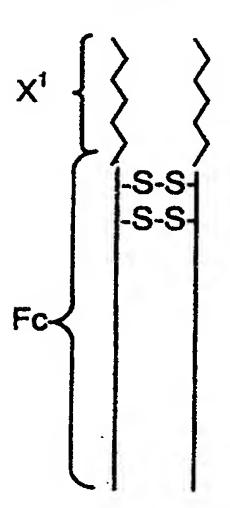


FIG. 3A

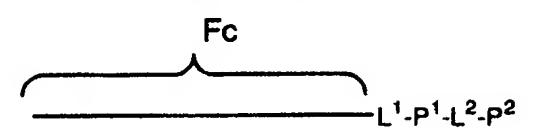


FIG. 3B

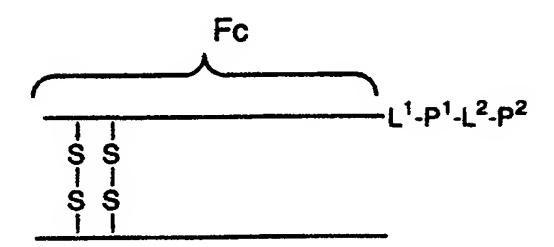
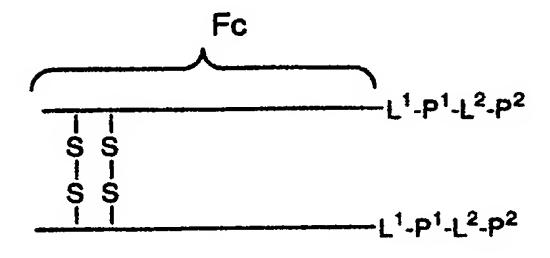


FIG. 3C



4/37 FIG. 4

	1	AT	GGA	CAA	AACT	rca(CAC	ATG				rcc?						GGC	GG!	CCC	TCA	60
	1	TA	CCT	GTTI	rtga	AGT	GTG	rac <i>i</i>										ccc	CC	rGGC	AGT	80
a		M	D	ĸ	T	H	T	С	P	P	С	P	A	P	E	L	L	G	G	P	S	-
	61																				GTC	120
	0.1												•								CAG	120
£		V	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P	E	V	•
	121		ATG				-	•										AAC	TGG	TAC	GTG	180
	121																	TTC	ACC	ATG	CAC	100
a		T .	С	v	V	V	D	V	S	H	E	D	P	E	V	K	F	N	W	Y	V	•
-	181		CGG														CAC				ACG	240
	TOT				•							•			-			-			TGC	220
3.		D	G	v	E	V	Н	N	A	K	T	K	P	R	E	E	Q	Y	N	S	T	-
	241	TAC	CCG!	rgte	GTC	CAGO	CGT	CTC	CAC	CGT	CCT	CAC	CAC	GA C	CTGC	CTC	CAA	'GGC	AAC	GAG		300
	471	AT	GGC2	ACAC	CAC	TCC	3CA(GA (GTG(GCA(GGA(CGTO	GTC	CTC	BACC	CGAC	CTTA	CCG	TTC	CTC	ATG	
a		¥.	R	V	V	S	V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	•
	301		GTG														ACC	ATC	TCC	AAA.	GCC	360
		TT	CAC	3TTC	CAC	BAG	3TTC	3TTI	rcg	GGA(GG?	rcge	3GG(STAC	CTC	TT	rtge	TAG	AGG	TTT	CGG	
a		K	C	K	V	S	N		A	_		A				K	T	I	S	K	A	-
	361	• •	• • •		+ -			+-				<u>-</u>	• • • • ·		+			-+-			ACC	420
		TT	TCC	CGTC	CGGC	GC1	rcti	rggi	rgt(GAC	TGG	
ā		K	G	Q	P	R	E	P	Q	•		T			P	S			Е	L	T	•
	421		• • •		+	• • •		+-				-			+			-+-				480
			CTT	GGT(TC(3GA(CTGC —	JAC(GGA(_				_	_	FTAG			
a		K	N	Q	V	5	L raac	T.	C 700/		V 3220	K	G mac		Y	P	S	D rece	ተ ተ	••	V GAC	-
	481				+		. <i></i> .	+ -			+				+	• • • •		-+-		• • •	GAC +	540
			-0-														.GGA				CTG D	-
3.		_	W	_	S			-	P ma	_											CAG	
	541				+			+-							++ -			-+-			GTC	600
_			GCT(D														s			_	0	•
2		_		_	_				·											-	AAG	
	601				+			+										-+-	•		TTC	660
a		_	N N														н				K	•
			CCT																			
	661		GGA		+	• • •		+ -		- (584											
																					•	

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FIG. 5 NH-Dde Pbf LRQWLAARA-GGG-HN CO-GGGG-IEGPTLRQWLAARA-OCH2 Pbf Boc Pbf Boc tBu Wang resin 2% H₂NNH₂/NMP Pbf Boc-IEGPTLRQWLAARA-GGG-HN Pbf Boc tBu Pbf Boc (BrCH₂CO)₂O Wang resin Boc-IEGPTLRQWI `CO-GGGG-IEGPTLRQ Pbf Boc Pbf Boc tBu Wang resin **TFA** H-IEGPTLRQWLAARA-GGG-HN CO-GGGG-IEGPTLRQWLAARA-OH peptide 17b MeO- PEG 5000 -SH MeO- PEG 5000 H-IEGPTLRQWLAARA-GGG-HN CO-GGGG-IEGPTLRQWLAARA-OH peptide 19

XbaI

FIG. 7

		 TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC	
c	1	AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG M D K T H T C P	60
	61	CACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAC GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGGTTTTG	120
C		PCPAPELLGGPSVFLFPPKP	•
c	121	CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT K D T L M I S R T P E V T C V V V D V S	180
		GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG	
C.	181	CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC H E D P E V K F N W Y V D G V E V H N A	240
	241	CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA	300
c		GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT K T K P R E E Q Y N S T Y R V V S V L T	•
	301	CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG	360
C		GGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTC V L H Q D W L N G K E Y K C K V S N K A	-
	361	CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC	420
C		GGGAGGGTCGGGGGTAGCTCTTTGGTAGAGGTTTCCCGTCGGGGGCTCTTGGTG L P A P I E K T I S K A K G Q P R E P Q	•
_	421	AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT **TCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA V V T L P P S R D E L T K N O V S L T C	480
C		GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC	
C	481	CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCG L V K G F Y P S D I A V E W E S N G Q P	540
	541	CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT	600
C		GCCTCTTGTTGATGTTCTGGTGCGGAGGGCCCGACGACCTGAGGCTGCCGAGGAAGAAGGAGA ENNYKTTPPVLDSDGSFFLY	•
	601	ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG TGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC	660
C		S K L T V D K S R W Q Q G N V F S C S V	•
	661		720
C		ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT M H E A L H N H Y T Q K S L S P G K	•
	721	AAGGTGGAGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGC	780
C		G G G G I E G P T L R Q W L A A R A *	•
		BamHI	
	781	AATCTCGAGGATCC	

	X.	1 1								-											
		TCTA	GAT'	rTG'	TTT	TAA	CTA	ATT	AAA	GGA(GA	ATA	ACA	TAT	GGA	CAA	AAC	TCA	CAC	ATGTO	
	1	AGAT	CTA	AAC	AAA	ATT(GAT!	raa:	rtt(CCT	CCT	rat	TGT	ATA	CCT	GTI	TTG	AGT	GTG	TACAC	· 60
C														M	D	K	T	H	T	CE	-
	C1	CACC	rtg:	rcc	AGC'	TCC	GGA	ACT	CCT	3GG(GG.	ACC	GTC.	AGT	CTT	CCI	CTT	CCC	CCC.	AAAAC	120
	61	GTGG	AAC	AGG'	TCG	AGG	CCT	rga	GGA (CCC	CCC	rgg	CAG	TCA	GAA	GGA	GAA	GGG	GGG	TTTTG	
C		P	C	Þ	A	P	E	L	L	G	G	2	\$	V	F	L	F	P	P	KF	-
		CCAA	GGA(CAC	CCT	CAT	GAT(CTC	CCG	GAC	ccc	rga(GGT	CAC	ATG	CGT	'GGT	GGT	GGA	CGTGA	
	121	GGTT	CT	+ GTG(GGA(GTA(CTA	GAG	GC(CTG	GG.	ACT	CCA	GTG'	TAC	GCA	CCA	CCA	CCT	GCACI	180
C		K	D	T	L	M	I	3	R	T	P	E	V	T	C.	V	V	V	D	V S	•
	404	GCCA	CGA	AGA	CCC'	TGA	GT(CAAC	3TTC	CAAC	TG	GTA(CGT	GGA	CGG	CGT	'GGA	GGT	GCA	TAATG	
	181	CGGT	GCT.	rct(GGG/	ACT	CCA	GTT	CAAC	TT(BAC	CAT	GCA	CCT	GCC	GCA	CCT	CCA	CGT.	ATTAC	240
C		H	E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N A	-
	044	CCAA	GAC	AAA	GCC	GCG	GA (3GA(GCA (TA(CAAC	CAG	CAC	GTA	CCG	TGT	GGT	CAG	CGT	CCTCA	300
	241	GGTT	CTG:	rtt(CGG	CGC	CCT	CTC	CGT	CATO	TT	STC	GTG	CAT	GGC	ACA	CCA	GTC	GCA	GGAGI	
C		K	T	K	P	R	E	E .	Q	Y	N	S	T	Y	R	V	V	3	V	L I	-
·			CCT	GCA(CCA	GGA(CTG	CT(GAAT	rgg(CAAC	GA (GTA	CAA	GTG	CAA	GGT	CTC	CAA	CAAAG	
	301		GGA(CGT	ggt(CCT	GAC	CGAC	CTT	ACC	TT(CT	CAT	GTT(CAC	GTT	CCA	GAG	GTT(GTTTC	360
C		v	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K	V	3	N	K A	•
		CCCT					_													ACCAC	
	361					GTA(•				-		TGGTG	
C					p													R		b Ö	
		AGGT	GTA(CAC	CCT	GCC	CCC	ATC	CCGC	G A1	rga(
	421	TCCAC	CATY	+ GTG(GGA	CGG/	GG7	rag(GCC	CTA	CTO									+ CTGGA	
C			Y	T		P												S		T C	•
		GCCT	GT(CAA	AGG	CTT	TA?	rcco	CAGO	GAC	ATC	CGC	CGT	GGA	GTG	GGA	GAG	CAA'	rgg	GCAGC	540
	481		CAC	GTT	rcc	GAAC	IAT	AGG	STC	CTC	TAC	3CG(GCA (CCT	CAC	CCT	CTC	GTT.	ACC	CGTCG	
C		L	V	K	G	F	Y	P	3	D	I	A	V	E	W	E	S	N	G	Q P	•
		CGGA	GAAC	CAAC	CTA	CAAC	GAC	CACC	3CC1	rccc	GTO	CTC	GGA (CTC	CGA	CGG	CTC	CTT	CTTY		600
	541		CTT	TTC	GAT(GTT	CTG	TG	:GG/	\GG(CAC	CGAC	CT	GAG	GCT ^o	GCC	GAG	GAA	GAA	GGAGA	
C		E	N	N	¥	K	T	T	P	P	V	L	D	3	D	G	S	F	F	L Y	-
	601		CAAC	CT(CAC	CGT	GA(AAC	SAGO											CTCCG +	
	801	TGTC								TCC	ACC	CGT	CGT	CCC	CTT	GCA	GAA	GAG'	rac	GAGGC	
C		S	K	L	T	V	D	K	S	R	W	Q	Q	G	N	V	F.	3	C	s v	•
	661	TGAT															CCT			GGGTA	
	991	ACTA	CGT	ACT	CCG	AGAC	CGT	TTC	GTG	ATC	TGO	CGT	CTT	CTC	GGA	GAG	GGA	CAG	AGG	CCCAT	
C		M	H	E	A	L	H	N	H	Y	T	Q	K	S	L	S	L	3	P	G K	•
		AAGGT																			
	721	TTCC	ACC	+ · rcci	ACC	ACC2	ATA(CTI	fCC)	\GG(TG	\GA(CGC	agt(CAC	CGA	CCG	ACG.	AGC.	ACGAC	780
C		G	_	_	G	G	I	E	G	P	T	L	R	Q	W	L	A	A	R	A G	•
	<u> </u>	GTGGT															ATG				
	781	CACC															TAC	-		+ TCGTG	
C			G		_															A R	
					В	amH:	.														
		GCGC	AŤA	ATC:	rcg	AGG/	ATC	CG													
	841			+			- ~ ~ ~	- {	361												

CGCGTATTAGAGCTCCTAGGC

	}	paI	
c	1	CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTC AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACTAGCTTCCAGGCTGAG M I E G P T L	+ 60
c	61	TCAGTGGCTGGCTGCTGCTGGCGGTGGTGGCGAGGGGGGTGGCATTGAGGGCCGCACCACCGACCG	+ 120 GTT
c	121	CCTTCGCCAATGGCTTGCAGCACGCGCAGGGGGAGGCGGTGGGGACAAAACTCACAG GGAAGCGGTTACCGAACGTCGTGCGCGTCCCCCTCCGCCACCCCTGTTTTGAGTGTG L R Q W L A A R A G G G G D K T H T	+ 180
c	181	TCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTTTTCCTCTTCCCCCCCC	+ 240
c	241	AACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGT PTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCACCACCACCACCACCACCACCACCACC	+ 300
c	301	GAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCACTCCACGTCGGTGCTGCTGCGCGCGC	+ 360 TAT
С	361	ATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG +	+ 420 AGG
c	421	CACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAI AGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGT T V L H Q D W L N G K E Y K C K V S N	+ 480 TGT
c	481	AAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAGCCCCCGAGAAGCCCCCAGAGAGCCAAAGGGCAGCCCCGAGAAGCCCCCGAGAAGCCCCCAAAGCCAAAGGGCAGCCCCGAGAAGCCCCCGAGAAGCCCCCAAAGCCAAAGGGCAGCCCCGAGAAGCCCCCAAAGCCCAAAGGGCAGCCCCGAGAAAGCCATCTCCGGGGCAGCCCCGAGAAAGCCATCTCCGAGAAAGCCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAAGCCATCTCCAAAAGCCAAAGGGCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAAAGCCATCTCCGAGAAAACCATCTCCAAAAGCCAAAAGCCAAAGGCCAAAGGCCAAAGGCCAAAGCCCCCGAGAAAGCCCAAAGCCAAAGGCCAAAGGCCAAAGGCCAAAGGCCAGAGAAAGCCATCTCCAAAAGCCAAAAGCCAAAAGCCAAAAGCCAAAAGCCAAAAGCCAAAAGCCAAAAGCCAAAAGCCAAAAGCCAAAAGCCAAAAGCCAAAAGCCAAAAGCCAAAAGCCAAAAGCCAAAAAA	+ 540 TTG
c	541	CACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCC' GTGTCCACATGTGGGACGGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGG Q V Y T L P P S R D E L T K N Q V S L	TGA + 600 ACT T -
c	601	CTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTAC C L V K G F Y P S D I A V E W E S N G	+ 660
c	661	AGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCT CCGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGA P P N N Y K T T P P V L D S D G S F F	+ 720 AGG
c	721	CTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATC AGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTAC Y S K L T V D K S R W Q Q G N V F S C	+ 780 CGA
С	781	CCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGCACATGCTACGTACTCCGGAGAGGGACAGAGGCACAGAGGCATGTGCGTCTTCTCGGAGAGGGACAGAGGV M H E A L H N H Y T Q K S L S L S P	+ 840 GCC
		Bamhi	
	841	GTAAATAATGGATCC	

GTAAATAATGGATCC 41 ----- 855 CATTTATTACCTAGG K *

	•	ADAI	
		TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC	•
-	1	AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACTAGCTTCCAGGCTGAGACG M I E G P T L R	U
С	61	GTCAGTGGCTGGCTGGTGGTGGAGGCGGTGGGGACAAAACTCACACATGTCCAC + 1 CAGTCACCGACCGACGAGCACGACCACCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTG	20
C		QWLAARAGGGGGDKTHTCPP-	
c	121	CTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTTTTCCTCTTCCCCCCAAAACCCA GAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGGTTTTGGGT C P A P E L L G G P S V F L F P P K P K	.80
	181	AGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCC	40
c	101	TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCACCTGCACTCGG DTLMISRTPEVTCVVVDVSH-	
	241	TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT	00
C		AGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCG	
c	301	TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC T K P R E E Q Y N S T Y R V V S V L T V	60
c	361	TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC AGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGG L H Q D W L N G K E Y K C K V S N K A L	2 0
c	421	TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCC PAPIEKTISKAKGQPREPQV	80
c	481	TGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCC ACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGG Y T L P P S R D E L T K N Q V S L T C L	40
	541	TGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG ACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCC	00
C		V K G F Y P S D I A V E W E S N G Q P E - AGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACA	
C	601		60
c	661	GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA CGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACT K L T V D K S R W Q Q G N V F S C S V M -	20
-	721	TGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAT	80
С		ACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTA H E A L H N H Y T Q K S L S L S P G K * - Bamhi	
	781	AATGGATCC 1 789	

TTACCTAGG

FIG.11

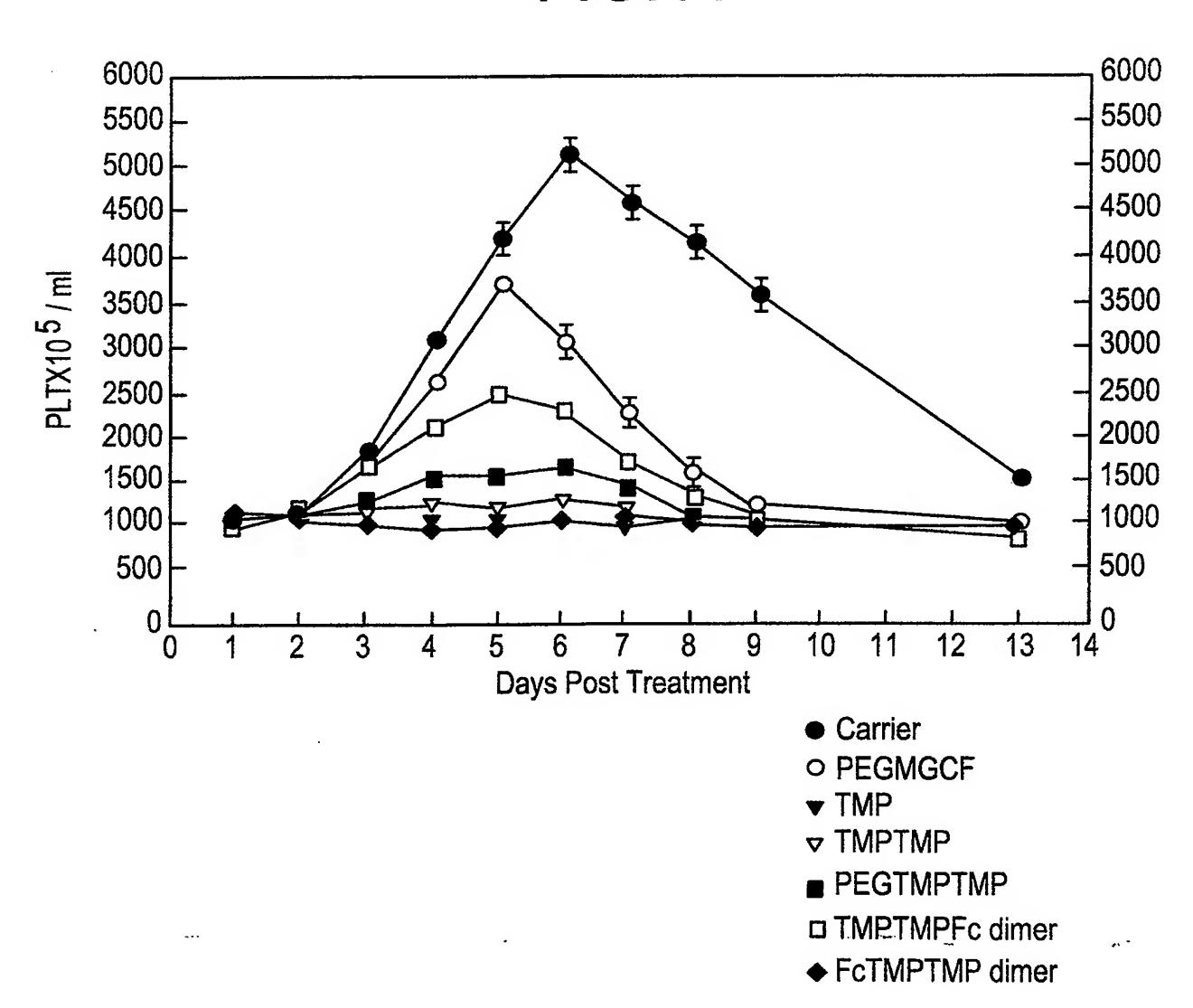
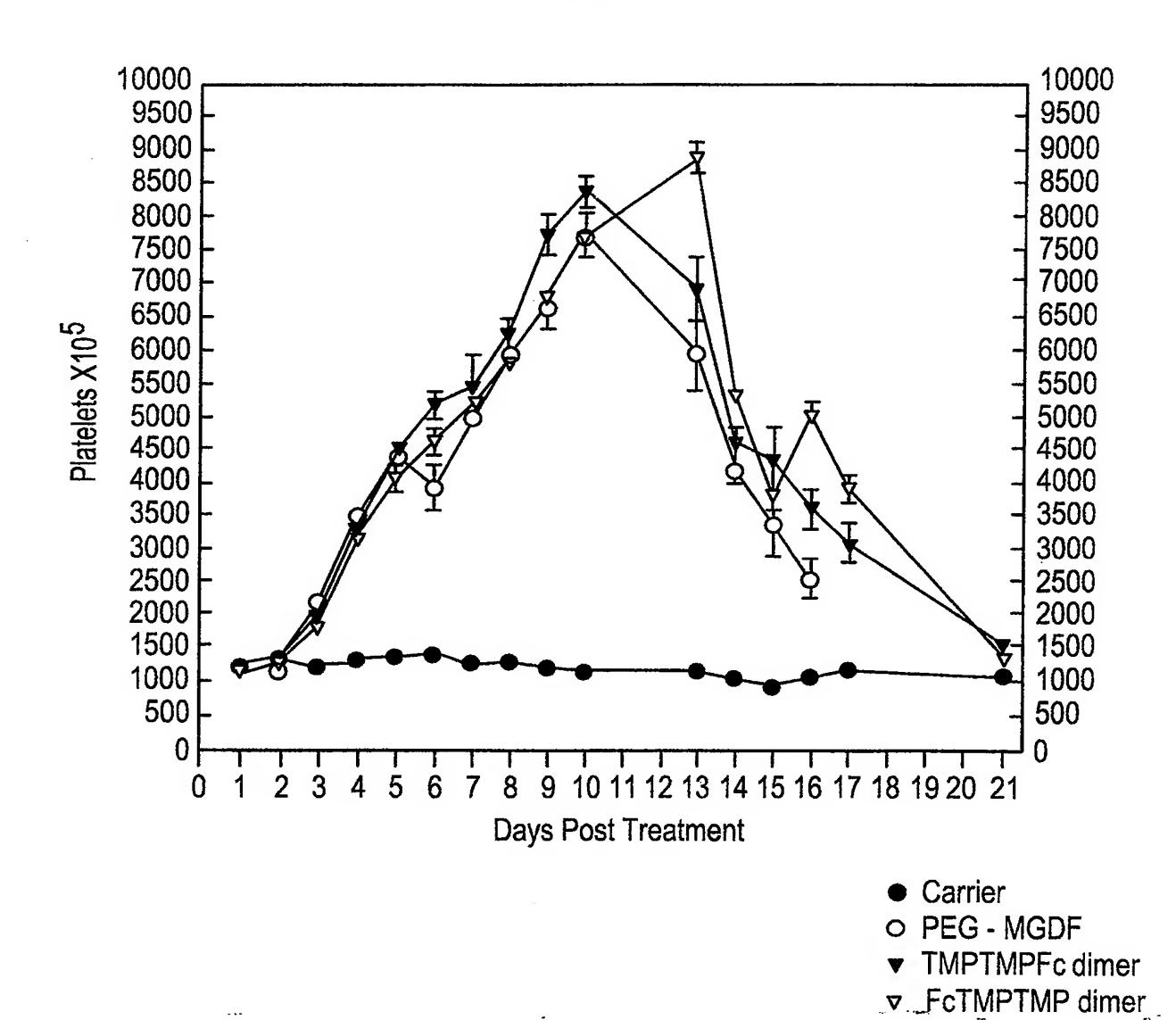


FIG.12



	2	(baI								E		•	ı							
	1	TCTAGAT	TTG	TTTI	CAAC	TAA	ATTA	AAC	3GA(GGA - + -	ATA	ACA	TAT	GGA	CAA	AAC'	TCA(CAC	ATGTC	60
c	•	AGATCTA											M	D	K	T	H	T	C P	_
	61	CACCTTO	+	· · - ·		+			• • •	-+-	• • •		+				+ ·		+	120
¢		P C	P	A	P	E	L	L	G	G	P	S	V	F	L	F	P	P	K P	
	121	CCAAGG	+			+				-+-	- • •		+		- • •		+		+	180
c		GGTTCC1 K D	T T	GGA(L	M	I I	S S	R	T		E	V	T	C.		V	V	D	V S	-
	181	GCCACGA	+	 .		+				-+-		•	+	• • •			+	• • •	+	240
c		CGGTGCT H E	TCT D	GGG <i>I</i> P	ACTO E	V	K K	F	N N	GAC W	CAT(Y	GCA V	CCT D	GCC G	GCA V	CCT E	V V	CGT. H	ATTAC N A	•
	241	CCAAGAC	+			+				-+-		•	+	• • •			+	• • •	+	300
c		GGTTCT(TTT K	CGG(P	CGCC R	E E	E E	GT(Q	CAT(Y	GTT N	GTC(S	GTG T	CAT Y	GGC. R	ACA V	CCA V	GTC S	GCA V	GGAG'I L T	
	301	CCGTCCT	+			4				-+-		• • •	+				+	• • •	+	360
c		GGCAGGI V L	ACGT H	GGT(Q	CTC D	W W	EGAC L	TTI N	ACC(GTT K	CCT(E	CAT Y	GTT K	CAC	GTT K	CCA V	GAG S	GTT N	GTTTC K A	-
	CC 361	CTCCCAG	cccc	CAT	CGA	GAA	AAC	CAT	CTC		AGC								AC	420
C	301	GGGAGGC L P	TCG A	GGG(P	GTAG I	E E	TTT K	TG(GTA(GAG S		TCG A	GTT K	TCC G	CGT Q	CGG P	GGC' R	TCT E	TGGTG P Q	;
	421	AGGTGT	ACAC	CCT	3CCC	CCA	ATCO	CGC	GGA'	TGA - + -	GCT	GAC	CAA	GAA	CCA	GGT	CAG	CCT	GACCI	480
C	421	TCCACAT V Y	_	GGA(CGGC P	GGT P			CCT. D		_		GTT K	CTT N	GGT Q	CCA V	GTC S	GGA L	CTGGA T C	•
	481	GCCTGG	rcaa + +	AGG(CTTC		rccc			CAT	CGC	CGT	GGA	GTG	GGA	GAG	CAA'	TGG	GCAGC	540
c		CGGACCI	K	G	F	Y	P	S	D	I	A	V	E	W	E	S	N	G	Q F	•
	541	CGGAGA	+			• • • •				-+-	•		+		• • •	• • •	+			- 600
C		E N	N	Y	K	T	T	P	P	V	L	D	S	D	G	S	F	F	L Y	! - 1
	601	TGTCGT	+	GTG	• • • •	+				-+-			+		• • •		+		GAGGO	660
C		S K		T	V	D	K	S	R	W	Q	Q	G	И	V	F	S	C	S V	•
	661		• • • +	GGC'			-			-+-	CGT		+	• • •	• • •		+ CAG	.		720
c		ACTACG	E	A	L	Н	N	H	Y	T	Q	K	S	L	3	L	S	P		.
	721		+	TGG'	TGG?	rggi	AGG:			-+-	• • •		+			• • •	+		CCAA	780
C		TTCCAC(G	G	G	G G	G	T	Y	S	C	H.	F	G	P	L	T	W	V (3 -
									Bam 	HI										
	781	GCAAAC	CGCA	'GGG	TGG:	TTA	ATC:	rcg	TGG	ATC	_	12								
	/01	CGTTTG	GCGI	CCC	ACC	AAT'	TAG	AGC.	ACC	TAG										

	X	ChaI							ŧ) .									
	1	TCTAG				+				+	• • •		+ -	• • •	• • •	• • •	+	•	+	60
2		AGATC											M	G	G	T	Y	5	C H	-
	61	ACTTCO TGAAGO		 -		+		• • •		+			+-				+		+	120
C			G P	L	T	W	V	C	K	P	Q	G	G	G	G	G	G	G	D F	•
c	121	TTTGAC				'GGA	ACG	GGI		+ 'GGA			+ -				+		1	180
	181	TCTTC	CCCC	CAAA	ACCO	AAG	GAC	ACC	CTC	ATG	ATC	CTC	CCGC	SAC	CCC	rga	GGT(CAC	ATGC	- 240
C	101	AGAAG(GGG(STTT. K	rggg P		CTG D	TGG T	GAG L	TAC M	TAC	Sag(GGCC R	CTG(T	GGG/ P	ACT E	CCA(V	GTG: T	TACG(C \	-
	241	TGGTGG	- 			+				+			+ -				+			- 300
C		•	ם ע	V	3	H	E	D	P	E	V	K	F	N	W	Y	V	D	G 1	•
~	301	ACCTC			ACGG	+	TGT		GGC	+	- + -		- ++	• • •			+		4	- 360
G	361	TGGTC	• • •				_						•	rgg(CAA	GGA	GTA(CAA	GTGC!	420
c	J 01	ACCAG:	rcgc) s v	AGGA(GTGC T	CAG V		GTG H	GTC Q		W W	CGA(CTTA N	ACC(G	TTY K	CCT E		GTT(.K	CACGI C I	
	421	AGGTC'				+				+ TAG	CTC	TT	rtg(TA(GAG	GTT	+	GTT	TCCC	480
C		V S	s n Cgagi	K AACC		L GTG	-	A ACC	P CTC	_	E	K ATC	T CCG(I GA:	s rga(k GCT	A GAC(k Caa	G (} -
C	481	TCGGG	GCTC:	rtgg' P	TGTC Q	CAC V	ATG Y	TGC T	GAC L	GGG P	GGT P	rag(GGC(CCT/ D	ACT(CGA L	ctg T	GTT(K	CTTG(540 3 2 -
	541	AGGTC		+		🕂				. +			+	• • •			+			- 600
C			S L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E	WI	z -
_	601	TCTCG'	TTAC	+ CCGT	cec	CTC	TTG			· + 3TTC	• • •		+		.	CGA	+		* * * * *	660
C		GCTCC'	-	Q FCCT	P CTAC	CAGO	:AAG	CTC	CACC	• •	- GA(CAA	GAG	CAG	GTG		_	GGG	GAAC	; + 720
c	661	CGAGG	AAGA F F	AGGA L	GAT(Y	STC G	TTC	GAÇ	FTG (CAC	CTO	GTT	CTC	GTC	CAC	CGT Q	CGT	9333 - B	CTTG(- N \	2 -
	721	TCTTC'	AGTA(+ CGAG	GCA	···+	GTA	CTC	CCG	- + - ·		GTT	+				+		• • • • •	780 1
C		F	s c	\$	V		H SamH		A	L	n	14	n	1	•	¥	K		Δ,	
	781		- +	+	• • •	4			{	307										
C		GGGAC. L	AGAG S P	_	ATT? K	rati	racc	TA(3 G											

^{15/37} FIG. 15

	XI	baI
	1	TCTAGATTTGAGTTTTAACTTTTAGAAGGAGGAATAAAATATGGGAGGTACTTACT
þ		M G G T Y S C -
b	61	CCACTTCGGCCCACTGACTTGGGTTTGCAAACCGCAGGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGC
	121	TACCTATTCCTGTCATTTTGGCCCGCTGACCTGGGTATGTAAGCCACAAGGGGGTGGGGG ATGGATAAGGACAGTAAAACCGGGCGACTGGACCCATACATTCGGTGTTCCCCCACCCCC
þ		T Y S C H F G P L T W V C K P Q G G G G AGGCGGGGGGGGGGGGGGGGGGGGGGGGG
þ	181	TCCGCCCCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCC G G G D K T H T C P P C P A P E L L G G
5	241	ACCGTCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCC TGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGG PSVFLFPPKFKDTLMISRTP
D	301	TGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG
þ		ACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGAC E V T C V V V D V S H E D P E V K F N W - GTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA
b	361	CATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCCTCCTCGTCATGTT Y V D G V E V H N A K T K P R E E Q Y N
b	421	CAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAA GTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTT S T Y R V V S V L T V L H Q D W L N G K
Б	481	GGAGTACAAGTGCAAGACCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
b		EYKCKVSNKALPAPIEKTIS CAAAGCCAAAGGGCAGCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGA
b	541	GTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACT K A K G Q P R E P Q V Y T L P P S R D E
b	601	GCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT + + + + + + + + + + + + + + + + + + +
b	661	CGCCGTGGAGTGGGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT + 720 GCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCA A V E W E S N G Q P E N N Y K T T P P V
	721	GCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG + 780 CGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCAC
Ъ	781	L D S D G S F F L Y S K L T V D K S R W - GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC 840
b		CGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTG Q Q G N V F S C S V M H E A L H N H Y T - Bamhi
b	841	CGTCTTCTCGGAGAGGGAGAGGCCCATTTATTACCTAGG Q K S L S L S P G K *
		SUBSTITUTE SHEET (RULE 26)

		Thai FIG. 16
	1	TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC
c		AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG M D K T H T C P
	61	CACCTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTTTTCCTCTTCCCCCCAAAAC
c	01	GTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGTTTTG PCPAPELLGGPSVFLPPPKP-
c	121	CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT K D T L M I S R T P E V T C V V V D V S ·
		GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATG
c	181	CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC H E D P E V K F N W Y V D G V E V H N A -
	241	CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA GGTTCTGTTTCGGCGCCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
C		KTKPREEQYNSTYRVVSVLT-
C	301	CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG GGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTC V L H Q D W L N G K E Y K C K V S N K A -
	361	CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
C		LPAPIEKTISKAKGQPREPQ-
c	421	AGGTGTACACCCTGCCTCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT **TCCACATGTGGGACGGAGGTAGGGCCCTACTCGACTGGTCCTGGTCCAGTCGGACTGGA V Y T L P P S R D E L T K N O V S L T C
	481	GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCG
C		LVRGFYPSDIAVEWESNGQP-
c	541	CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT + 600 GCCTCTTGTTGATGTTCTGGTGCGGAGGCACGACCTGAGGCTGCCGAGGAAGAAGAAGAAGA E N N Y K T T P P V L D S D G S F F L Y -
	601	ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGGAACGTCTTCTCATGCTCCG + 660
С		TGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC S K L T V D K S R W Q Q G N V F S C S V -
c	661	TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA + 720 ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT M H E A L H N H Y T Q K S L S L S P G K -
		AAGGTGGAGGTGGCGGAGGTACTTACTCTTGCCACTTCGGCCCACTGACTTGGGTTT
c		TTCCACCTCCACCACCGCCTCCATGAATGAGAACGGTGAAGCCGGGTGACTGAACCCAAA G G G G G T Y S C H F G P L T W V C
	781	GCAAACCGCAGGGTGGCGGCGGCGGCGGCGGTGGTACCTATTCCTGTCATTTTGGCCCGC CGTTTGGCGTCCCACCGCCGCCGCCGCCACCATGGATAAGGACAGTAAAACCGGGCG
C		KPQGGGGGGTYSCHFGPL-
		Bamhi TGACCTGGGTATGTAAGCCACAAGGGGGTTAATCTCGAGGATCC
	841	ACTGGACCCATACATTCGGTGTTCCCCCAATTAGAGCTCCTAGG
¢		T W V C K P Q G G *

FIG. 17A

[<u>Aat</u>II sticky end] (position #4358 in pAMG21)

- 5' GCGTAACGTATGCATGGTCTCC-
- 3' TGCACGCATTGCATACGTACCAGAGG-
- -CCATGCGAGAGTAGGGAACTGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT-
- GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGA -
- GGGCCTTTCGTTTATCTGTTGTTTGTCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC -
- -CCCGGAAAGCAAAATAGACAACAACAGCCACTTGCGAGAGGACTCATCCTGTTTAGGCG-
- CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCGC -
- GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCCTCCCACCGCCCGTCCTGCGGGCG-
- -CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTGCGT-
- GTATTTGACGGTCCGTAGTTTAATTCGTCTTCCGGTAGGACTGCCTACCGGAAAAACGCA -

AatII

- -TTCTACAAACTCTTTTGTTTATTTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC-
- AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG -
- TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAAATTGCTTTAGAAATACTTTGGCAGC -
- AAAATTTCATACCCGTTAGTTAACGAGGACAATTTTAACGAAATCTTTATGAAACCGTCG-
- -GGTTTGTTGTATTGAGTTTCATTTGCGCATTGGTTAAATGGAAAGTGACCGTGCGCTTAC -
- -CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCACTGGCACGCGAATG-
- TACAGCCTAATATTTTTGAAATATCCCAAGAGCTTTTTCCTTCGCATGCCCACGCTAAAC -
- ATGTCGGATTATAAAAACTTTATAGGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTTG -

- GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTCATACACGCATGTAAAAATA -
- -CTATTAATAGTTGATCTCTTCCTTGTTAATTACCATACAAGTATGTGCGTACATTTTTAT-
- AACTATCTATATAGTTGTCTTTCTCTGAATGTGCAAAACTAAGCATTCCGAAGCCATTAT -
- TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTCGTAAGGCTTCGGTAATA -
- TAGCAGTATGAATAGGGAAACTAAACCCAGTGATAAGACCTGATGATTTCGCTTCTTTAA -- ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAATT -
- TTACATTTGGAGATTTTTTTATTTACAGCATTGTTTTCAAATATATTCCAATTAATCGGTG -
- AATGTAAACCTCTAAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTTAATTAGCCAC -
- AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT -
- TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAAATAATTTAATCGCAGTAGTA -
- AATATTGCCTCCATTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG -
- TTATAACGGAGGTAAAAAATCCCATTAATAGGTCTTAACTTTATAGTCTAAATTGGTATC -
- AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG -
- -TTACTCCTATTTACTAGCGCTCATTTATTATAAGTGTTACATGGTAAAATCAGTATAGTC-

- GCAAGTTTTGCGTGTTATATATCATTAAAACGGTAATAGATTGACATTTGATTCTAATAA -
- -CGTTCAAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAAACTAAGATTATT-

FIG. 17B

- ATTGGATTTTTGTCACACTATTATATCGCTTGAAATACAATTGTTTAACATAAGTACCTG -
- TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC -
- TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGATTAATCGATTTGATT -
- ATCCTAGCATGTCCAAATGCGTTCTTTTACCAAACAATATCAGCTAATTAGCTAAACTAA -
- -CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA -
- GATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCT -

SacII

- -GCTCACTAGTGTCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA -
- -CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT-
- -GAAGAAGAAGAAGCCCGAAAGGAAGCTGAGTTGGCTGCCACCGCTGAGCAATA -
- CTTCTTCTTCTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT -
- ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGGTTTTTTTGCTGAAAGGAGG-
- TGATCGTATTGGGGAACCCCGGAGATTTGCCCAGAACTCCCCAAAAAACGACTTTCCTCC -
- AACCGCTCTTCACGCTCTTCACGC 3'

[SacII sticky end]

-TTGGCGAGAAGTG 5'

(position #5904 in pAMG21)

FIG.18A - 1

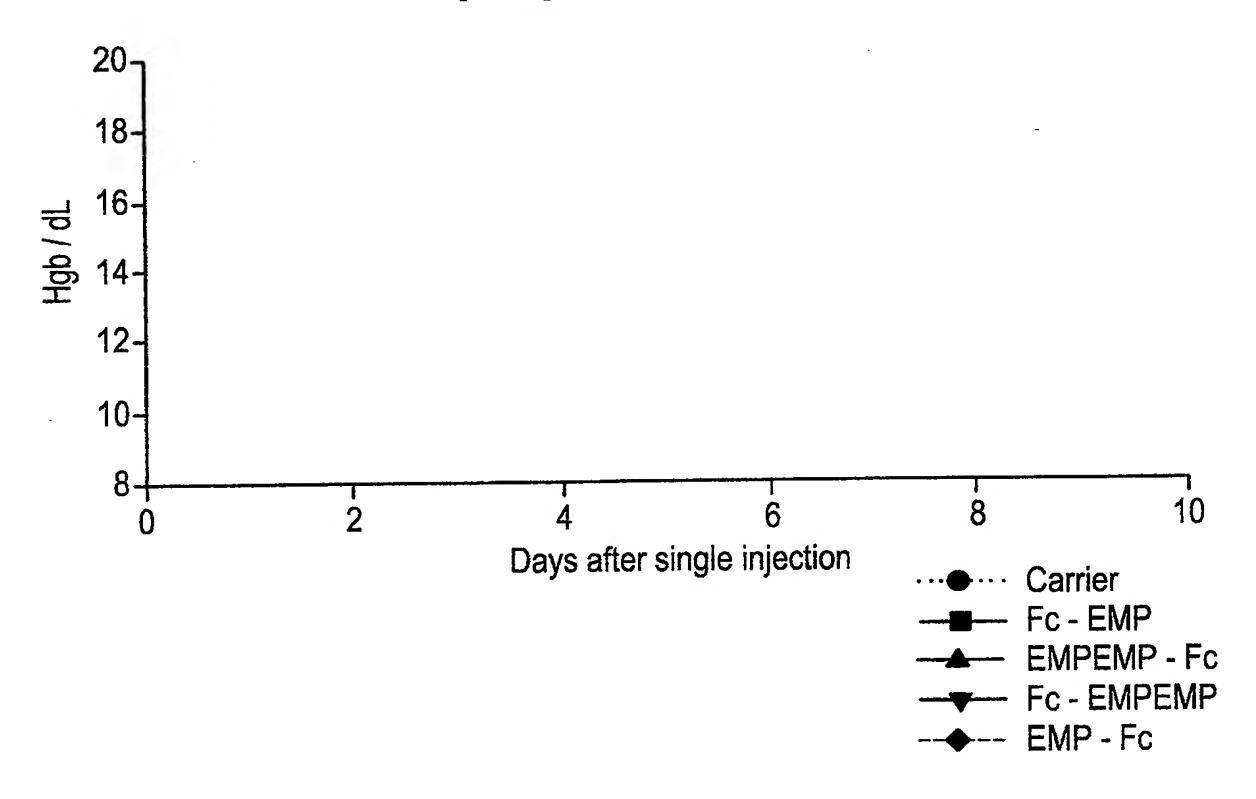


FIG.18A - 2

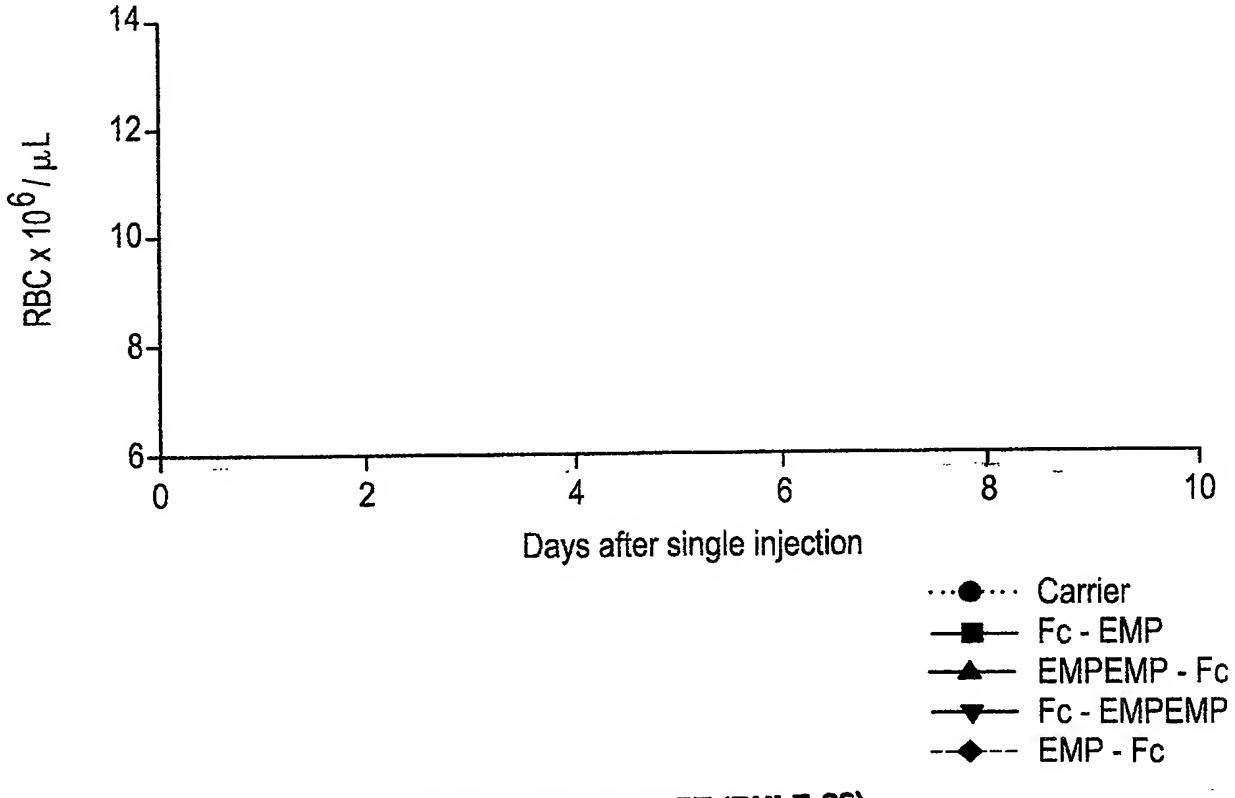


FIG.18A - 3

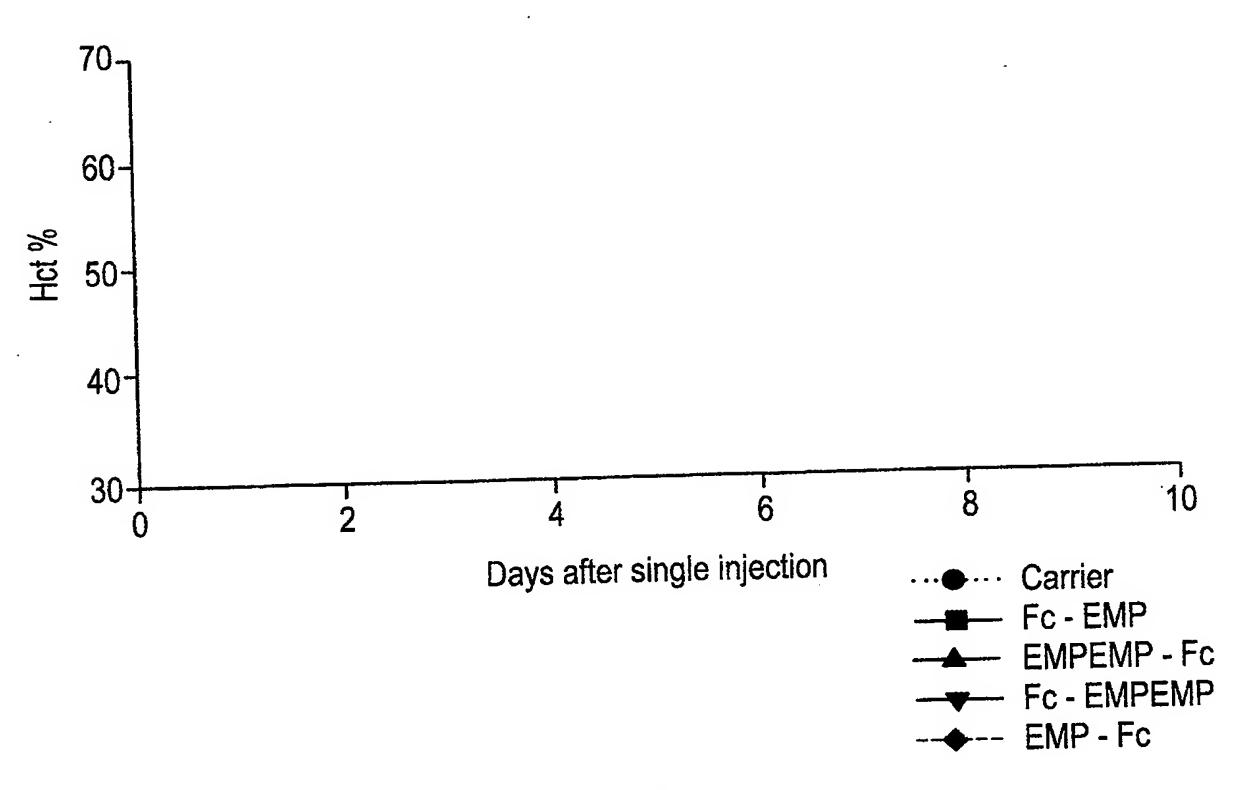


FIG.18B - 1

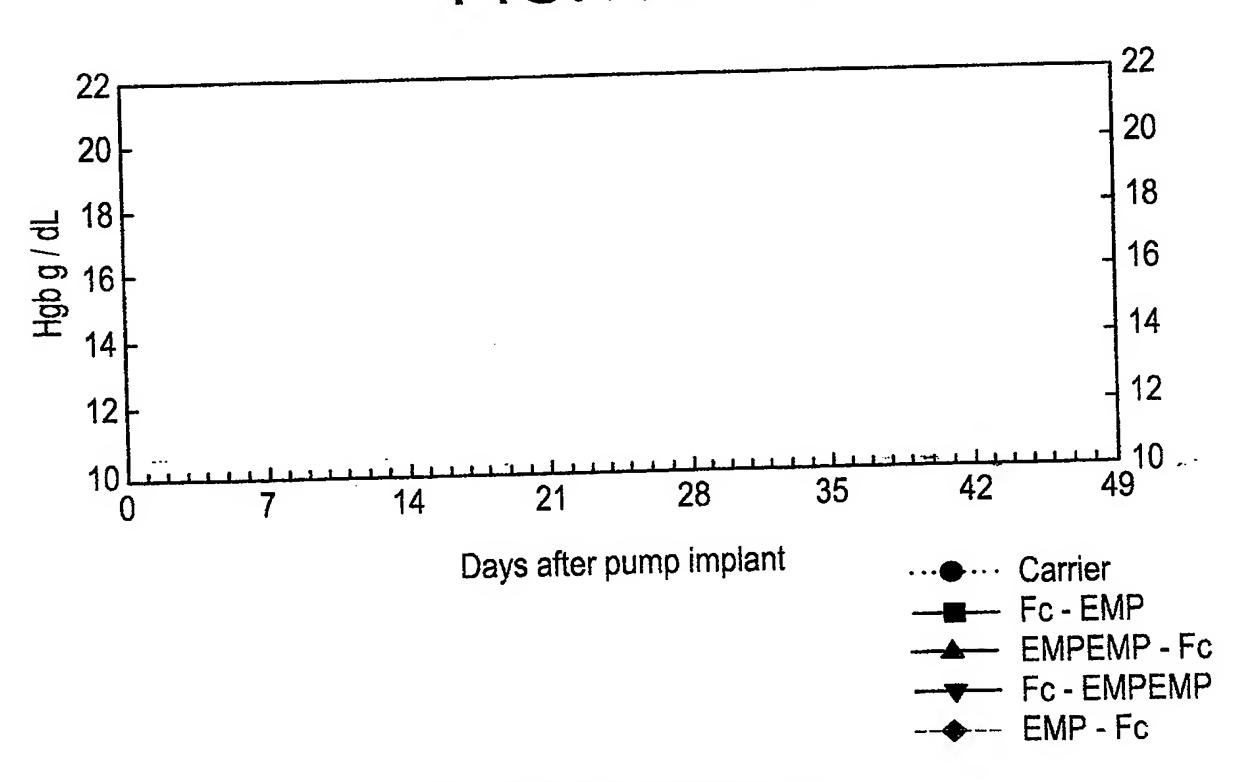


FIG.18B - 2

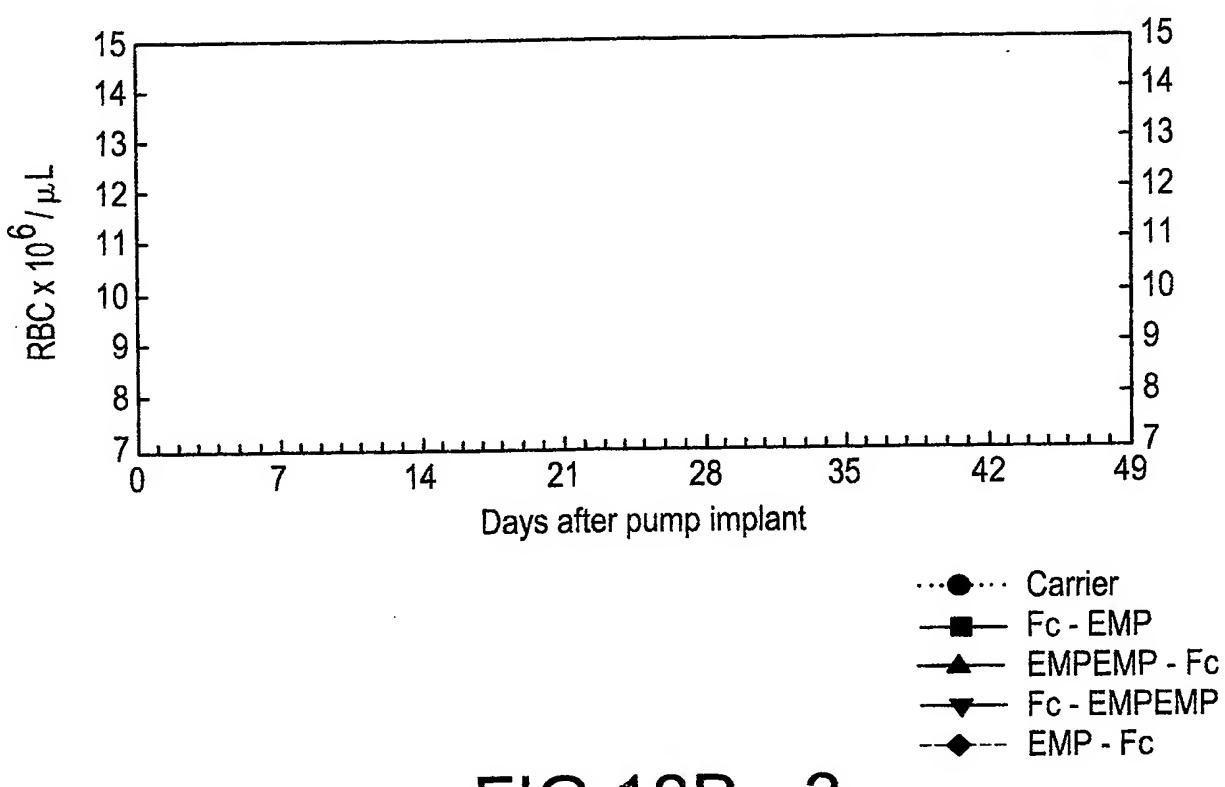


FIG.18B - 3

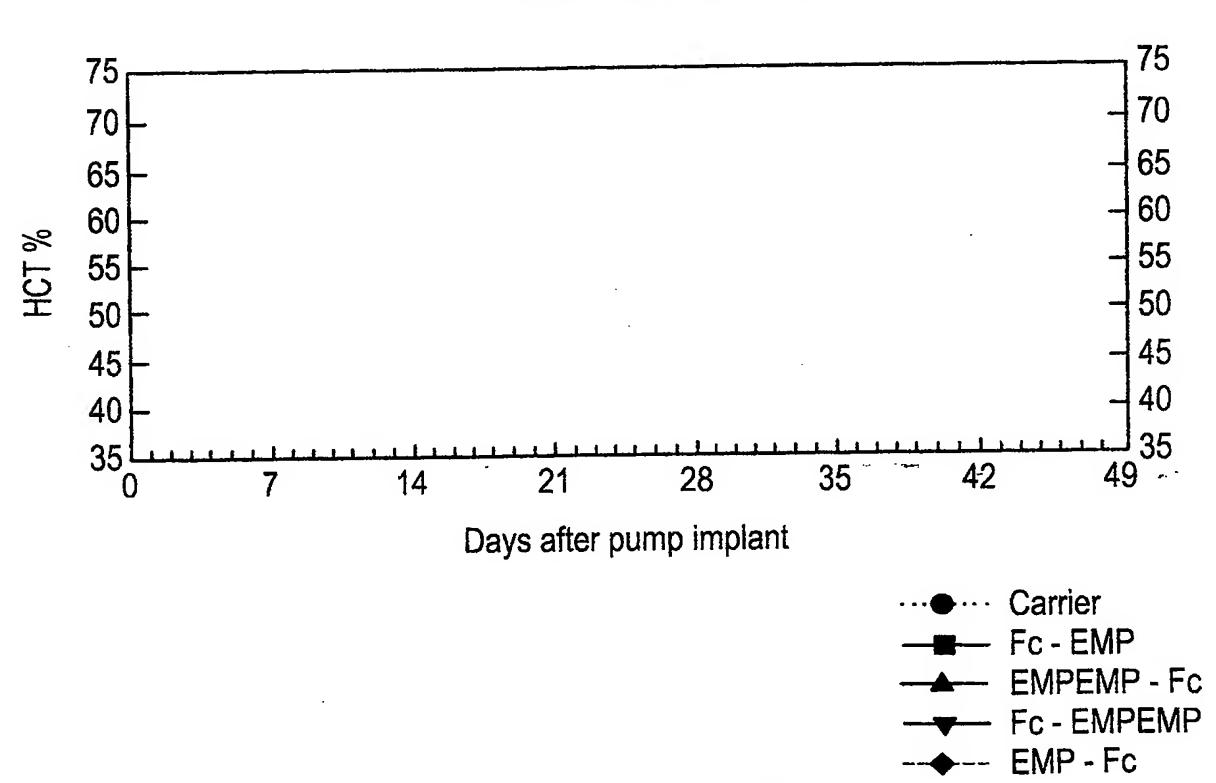


FIG. 19A

	NdeI								•			•	•	_								
	_	CAT			1			4							+	+		-			•	60
	±	GTA?	raco	CTG	TTI	TG	AGT(GTG1	raca	AGGT	rgga	ACA	\GGT	CGA	\GGC	CTT	'GAG	GAC	CCC	CCT	النان ا	
a		_	_		K	T	Н	T	С	P	P	C	P	A	P		L	L ·			P GlG	•
	-	TCA			Ł										. +						•	120
	61	AGT(CAG	AAG	GAC	3AAC	GG G	GGG!	rtt:	rgg(GTT(CCTC	TGC	GAC	STAC	CTAC	AGC	GCC	CTGG	GGA	CTC	
a			•	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P	E	•
		GTC	ACA'	TGC	GTC	GT(GGT	GGA	CGT	GAG	CCA	CGA	AGA	ccc	rga(GTC	CAAC	3TT(+ ·	CAAC	TGG	TAC	180
	121	CAG	TGT.	ACG	CAC	CCA	CCA	CCT	GCA(CTC	GGT	GCT'	CTC	GGG2	ACTO	CCAC	TTC	CAA	GTTG	ACC	ATG	
a		v	T ·	С	v	v	v	D	v	S	Н	E	D	P	E	v	K	F	N .	W	Y	-
		GTG	GAC	GGC	CGT	GGA	GGT	GCA	TAA'	TGC	CAA	GAC	AAA	GCC	GCG	GGA(GA (GCA	GTAC	CAAC	AGC	240
	181											+			- + - '						STCG	240
a				G	v	E	v	Н	N	A	K	T	K	P	R	E	E	Q	Y	N	S	•
u		እሮር	የጥል (*	ירניי	ኮርረጥ	ርርጥ	CAG	CGT	CCT	CAC	CGT	CCT	GCA	CCA	GGA	CTG	GCT	GAA	TGG	CAAC	GAG	
	241											+						+		•	CTC	300
		TGC	ATG	iGC:	ACA			_				_	Н	0	D	W		N	G	ĸ	E	-
a		T	Y	R	V	V	S	V	L	T	V	L	-	-						~m~(בגבי	
	301							1				-					=	•				360
	302	ATO	STTC	CAC	GTT	CCA	GAG	GTI	GTT	TCG	GGA	.GGG	TCG	GGG	GTA						GTTT	
a		Y	K	C	K	V	S	N	K	A		-	A		I	E	K	T	I	S	K	•
									L				-					1			GCTG +	
	361	CGC	3TTI	rcc	CGI	CGG	3GG(CTC	rTGC	TGT	CCA	CAT	GTG	GGA	CGG	GGG	TAC	GGC	CCT.	ACT	CGAC	
a		A	K	G	Q	P			P	Q	v	Y		L			S	R	D	E	L	•
		AC	CAA	GAA	CCA	\GG?	rca	GCC!	rgac	CTC	CC1	rgg1	CAP	AGC	CTT	CTA	TCC	CAC	CGA	CAT	CGCC +	480
	421	TG	GTT(CTT	'GG'	rcci	AGT(CGG	ACTO	GGA(CGG!	ACCA	GTI	rtcc	CGAA	\GA'I	AGC	GTC	GCT	GTA	GCGG	
a		T	K	N	Q	V	S	L	Т	С	L	V	K	G	F	Y	P	S	D	I	A	-
		GT	GGA	GTG	:GG?	AGA	GCA.	ATG	GGC	AGC	CGGI	AGA	ACA	ACTA	ACAA	AGAC	CAC	CGCC	CTCC	CGT	GCTG	540
	481								4						• • • •			,	•		CGAC	
3		v	E	W	E	_			-			N				•••		P		V	L '	~ ~
a		•	_	,, GG 2				_		MC III	አሮኔሪ	CC A	۸۵۵۰	TCA	CCG	rggi	ACA	AGA	GCA G	GTG	GCAG	;
	541				_				1						• • •				•		CGTC	
		CT.			_				_	Y		4.	_		v	_					Q	•
a		Ŋ	S	D	G	S	Ľ	Ľ		*	~			_								

FIG. 19B

a		K	N	T	S	L	G	Н	R	P	*											
	721				-+-			+	CCG		GT?	+	GAI		757	,						
a		K	S	L	S	L	S	P	G	K			G	G	G	D	F	L	P	H	Y	-
	661				- + -			+				+			-+-		• • •	+			GATG	120
a		Q	G	N	V	F	S	C	S	V سمم		H TGG								T GCA	Q CTAC	•
	601	GT	CCC	CTT	-+- GCA	GAA	GAG	+ TAC	GAG	GCA	CTA	.CGT	ACT	CCG	AGA	CGT	GTT	GGT	GAT	GTG	CGTC	000
		CA	GGG	GAA	CGT	CTT	CTC.	ATG	CTC	CGT	GAT	GCA	TGA	GGC	TCT	GCA	CAA	CCA	CTA	CAC	GCAG	660

FIG. 20A

		Nde																				
		 CAT <i>i</i>	ATG(GAC	TTC	CTO	ECC(GCA(CTA	CAA	AAA(CACC	TCI	CTG	GGT	CAC	CG	CCC	igg1	GGZ	AGGC	60
	1	GTA!	rac	CTG	+ AAG	GAC	CGG	+ CGT(GAT	GTT	TTT(GTG	AGA	GAC	CCA	GTG	GC <i>I</i>	AGĞ	CCA	ACC	rccg	
a		_	•		F	L	P	Н	Y	K	N	T	S	L	G	Н	R	P	G	G	G	-
								•	_					,		-		•			-	120
	ΟŢ	CCA	CCC	CTG	TTI	rtgi	AGT	GTG	TAC	AGG	TGG	AAC	GGG?	rcgi	rggi	ACTI	rga(3GA(JUU	rggc	
a		~	•	_	K	T	Н	T	С	P	P	С	P	A	P	E	L	L	G	G	P	•
															-			•			-	180
	121	AGT	CAA	AAG	+- GA	GAA	GGG	GGG	TTI	TGG	GTT	CCT	GTG	GGA	GTA	CTA	GAG	GGC	CTG	GGG	ACTC	
a		S	v	F	L	F	P	P.	K	P	K	D	T	L	M	I	S	R	T	P	E	-
		GTC	ACA	TGC	CGT	GGT	GGI	:GGA	CGI	GAG	CCA	CGA	AGA	CCC	TGA	GGT	CAA	GTT	CAA	CTG	GTAC	240
	181	CAG	 :тст	'ACC	+- CA	CCA	CCA	CCI	'GC	CTC	CGGI	GCT	TCT	GGG	ACT	CCA	GTT	CAA	GTT.	GAC	CATG	
a			T	C	V	V	v	D	V	S	Н	E	D	P	E	V	K	F	N	W	Y	-
•		ሪ ሞር	ica (raac	CGT	'GGA	\GG?	rgc <i>i</i>	\TAI	ATG(CCA	AGAC	AAA	GCC	GĊG	GGA	GGA	.GCA	GTA	CAA	CAGC	300
	241								t						- -	* .		•			rgtcg	
		CAC	CTC								K		K	P	R	E	E	Q	Y	N	s	-
a		V	D	G	V	E	V		_			_		_	.ccz	አርጥር	ige?	rga <i>i</i>	\TG(3CAI	AGGAG	
	301																					
	3 -	TG	CAT	GGC.	ACA	ACCI	AGT	CGC.	AGG.	AGT	GGC.	AGG/		_	_		_				rcctc e	*
a		T	Y	R	A	V	S	-	_	T	V		H	-	D	W	L		G		-	
									1 .				'						-		CCAAA	
	361	AT	GTT	CAC	GT.	rcc.	AGA	GGT	TGT	TTC	:GGG	AGG	GTC	GGG	igt:	AGC	rct'	TTT	GGT.	AGA	GGTTT	
a		Y	К	С	K			_	_						I	E				_	.	-
		GC	CAA	AGG	:GC	AGC	CCC	GAG	AAC	CAC	AGG	TGT	ACA	CCC'	rgc	CCC	CAT	CCC	GGG +	ATG	AGCTO	480
	421	CG	GTT	TCC	-+ :CG'	TCG	GGG	CTC	TTC	GTO	TCC	ACA	TGT	GGG	ACG	GGG	GTA	GGG	CCC	TAC	TCGAC	
a			K																		L	-
-		A C	'CAA	GAA	ACC	AGG	TCA	AGCC	TG	ACC?	rgcc	TGG	TCA	AAG	GCT	TCT	ATC	CCA	GCG	ACA	TCGC	540
	48																				AGCG	
											C I			. G			F				A	***
a			K		Q	•								ACT	'ACA	AGA	CCA	CGC	CTC	ccc	GTGCT	G
	54																					
		CZ	ACC!	rca	CCC	TCI	rcg'	TTA	CCC	GTC	GGC(J.I.C.	161	LUA	1101					p 1	_	-
a		Ÿ	E	W	E	E \$	5	N (G	Q	P !	E 1	1 1	1 <i>y</i>	r	ζ 🦪	<u>r</u> 7	r I		· '	v 44	

a

FIG. 20B

GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG

CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTTCTCTCGTCCACCGTC

D S D G S F F L Y S K L T V D K S R W Q

CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG

GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

Q G N V F S C S V M H E A L H N H Y T Q

BamHI

AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG

721

TTCTCGGAGAGGGCACAGAGGCCCATTTATTACCTAGGCGCC

FIG. 21A

		.e.i																				
	1	CATA						+ -							+			-+-			+	60
		GTA?	raco	CTG	TTT	TG	\GT(GTG?	raca	\GG1	'GG!	AACA	GGT	CGA	GGC	CTT	GAG	GAC	CCC	CUT	ناحات	
a		ì	M I	D	K	T	H	T	C	P	P	C	P	A	P	E	L	L	G	G	P	-
		TCA	GTC	TTC	CTC	TTC	ccc	CCC	AAAA	ACCO	CAAC	GAC	CACC	CTC	ATG +	ATC	TCC	CGG:	ACC	CCT	GAG	120
	61	AGT	CAG	AAG	GAC	SAAC	GG(GG:	rTTI	rgge	TTC	CCTG	TGG	GAG	TAC	TAG	AGG	GCC	TGG	GGA	CTC	
a		s ·	V 1	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P	E	•
•		GTC	ACA'	TGC	GT	GT(GT(GGA (CGT	GAGO	CAC	CGAA	GAC	CCT	'GAG	GTC	AAG	TTC	AAC	TGG	TAC	180
	121	CAG'	TGT	ACG	CAC	CAC	CCA	CCT	GCA	CTC	GT(GCT7	CTG	GGA	CTC	CAG	TTC	AAC	TTG	ACC	-	100
a		v '	T (C	V	V	v	D	V	S	Н	E	D	P	E	V	K	F	N	W	Y	-
		GTG	GAC	GGC	GTC	GGA(GGT(GCA'	raa:	rgc	CAA	GAC!	AAAG	CCG	CGG	GAG	GAC	CAC	STAC	AAC	AGC	240
	181	CAC	CTG	CCG	+- CAC	CCT	CCA	+ CGT/	ATT	ACG(3TT(-						GTC	CATG	TTG	TCG	
a					v	E	V	Н	N	A	K	T	K	P	R	E	E	Q	Y	N	S	••
_		ACG	тас	CGT	'GT(GGT(CAG	CGT	CCT	CAC	CGT	CCT	GCAC	CAG	GAC	TGG	CTC	AAT	rggc	AAG	GAG	
	241							+				+	• • • •		+			• • • •			CTC	300
a				R	v	v	S	V	L	T	V	L	Н	Q		W	L	N	G	K	E	-
ŭ.		_	AAG	TGC	'AA	GGT	CTC	CAA	CAA	AGC	CCT	CCC	AGC	CCC	CATC	GAG	JAA	AAC(CATO	TCC	AAA	260
	301				. . -	-		+			 -	+			• • • •						TTT	360
		ATG	rric	.ACC						_		P		P	I	E	ĸ	T	I	S	К	-
a		•	•	C	K	V	3	N	K	A				_	_			-	_			
	361				. 4 -			+				+			- +	•		+			•	420
	~ ~	CGG	TTT	CCC	CGT	CGG	GGC	TCT	TGG	TGT	CCA	CAT	GTG(GGA(CGG(3GG'	ľAG	GGCI	CCTA	ACTO	CGAC	
a		A	K	G	Q	P	R	E	P	Q	•	Y	T		P	P	S	R	D	E	L	•
	401	ACC	CAAG	AAC	CCA	GGT	CAG	CCT	GAC	CTG	CCI	GGT +	CAA	AGG(CTT(• + -	CTA!	rcc	CAG +	CGA	CAT	CGCC	480
	421	TGG	TTC	TT	GGT	CCA	GTC	GGA	CTG	GAC	GGA	CCA	GTT'	TÇC	GAA(SAT	AGG	GTC	GCT	GTA(GCGG	
a		T	K	N	Q	V	S	Ŀ	T	C	L	V	K	G	F	Y	P	S	. D	I	A	-
		GTC	GA C	3TG(GGA	GAG	CAA	TGG	GCA	GCC	GGA	GAA	CAA	CTA	CAA	GAC	CAC	GCC	TCC	CGT	GCTG	540
	481	CAC	 ССТО	CAC	- + - CCT	CTC	GTI	ACC	:CGI	CGG	CCI	CTT	GTT	GAT	GTT	CTG	GTG	CGG	AGG	GCA	+ CGAC	,. 9 4 0
a		V		W		S						N						p		٧		-
<u> </u>		CN	~m/~/	CA	CGG	יכיייכ	ئىلى <u>تا</u> سىلىكى	ւՇու	rcci	CTA	CAC	CAA	GCT	CAC	CGT	GGA	CAA	GAG	CAG	GTG	GCAG	
	541				. 4 -							• 💠			- + -						CGTC	000
		CT(_					K								W	Q	•
a		D	S	D	G	S	F	F	ىيا	I	3	~	Ļ		•		-				_	

FIG. 21B

															- -			•			GCAG	660
	601	GT	CCC	CTT	GCA	GAA	GAG	TAC	GAG	GCA	CTA	CGT	ACT	CCG	AGA	CGT	GTT	GGT	GAT	GTG	CGTC	
a		Q	G	N	v	F	S		•	V		Н	-	A	•	H		H	Y	T	Q	-
													~ ~ ~		- -			•			GGGT	
	661	TT	CTC	GGA	GAG	GGA	CAG	AGG	CCC	ATT	TCC	ACC	TCC	ACC	ACC	AAA.	GCT	TAC	CTG	GGG	CCCA	
a		K	S	L	S	L	S	P	G	K	G	G	G	G	G	F	E	W	T	P	G	•
												mHI 										
	721							TCI + BAGA				•			•		763	3				
3		Y	W	0	P	Y	A	L	P	L	*											

FIG. 22A

		Nd	eI																			
	_	CAT	'ATG	TTC	GA/	ATG	GAC	CCC	GGG'	TTA		GCA(CTO	CCC	CTC	GGI	GGA	.GGC	60
	1	GTA	TAC	AAC	CT:	rac	CTG	GGG	CCC	AAT		•			-	AGAC	CGGC	CGAC	CCA	CCI	CCG	
a			M	F	E	W	T	P	G	Y	M	Q	P	Y	A	L	P	L	G	G	G	•
	<i></i>	GGT	'GGG	GAC	CAAI	AAC	TCA	CAC	ATG	TCC	ACC'	TTG	CCC	AGC	ACCI	rgaz	ACTO	CTC	GGG	GGA	CCG	120
	61	CCA	CCC	CTC	TT	rtg	AGT	GTG	TAC.	AGG	TGG.	AAC	GGG:	rcg	rgg <i>i</i>	CTI	rgac	GA C	CCC	CC1	GGC	
a		G	G	D	ĸ	T	Н	T	С	P	P	С	P	A	P	E	L	L	G	G	P	-
		TCA	\GTI	rtt	CT	CTT	ccc	ccc	AAA	ACC	CAA	G GA (CAC	CCT	CATO	TAE	CTC	CGG	ACC	cci	GAG	180
٠	121	AGT	CA	AAA	GA(GAA	GGG	GGG	TTT	TGG	GTT	CCT	GTG	GGA	GTA	CTAC	GAG	GC(CTGC	GGA	CTC	100
a		s	v	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P	E	-
		GTO	CAC	ATG	CGT	GGT	GGT	GGA	CGT	GAG	CCA	CGA	AGA	CCC'	TGA	GT(CAAC	GTT(CAAC	CTGC	STAC	240
	181	CAC	GTG	rac	- + - GCA	CCA	CCA	+ CCT	GCA	CTC	GGT	+ 'GCT'	TCT	GGG.	ACT	CCA	GTT(CAA	GTT(BAC	CATG	240
a		V	T						v		Н			P		V	.K	F	N	W	Y	•
		GTO	GGA(CGG	CGT	GGA	GGI	GCA	AAT	TGC	CAA	GAC	AAA	GCC	GCG	GGA(GGA(GCA	STA (CAAC	CAGC	200
	241				- 4 -			+				+	• • •		-+-	- + -		+			TCG	300
3		v	D	G	v	E	V	н				T					E	Q	Y	N	s	-
a		` 	~m % (مصرة	ሞርጥ	പ്പ	CAC	ירניו	ነሮሮፕ	CAC	:CGT	CCT	GCA	CCA	GGA	CTG	GCT(GAA'	rgg	CAA	GGAG	
	301							4				+			-+-			+			CCTC	360
		T G	CMT.	90C	A\-A ₹7	77	S	v	_	T		L			D	W	L		G		E	-
а		T	Y	K	v ~~ ~	v com										CGA	GAA	AAC	CAT	CTC	CAAA	
	361							4	-			· +			-+-			+			GTTT	420
		AT	GTT	CAC	GTT							r P							I		ĸ	-
a		Y	K	С	K	V	S	N		A												
	421											. +			-+-		*	+				480
		CG	GTT	TCC	CGI	CGG	GG(CTC	rtgo	GTG:	rcc <i>i</i>	ACAI	GTG	IGGA	CGG	GGG	TAG	GGC	CCT		CGAC	
a			K		Q	-		E		Q		Y				P		R	D		L	•
	401		_						4			- + + -			-+-						CGCC	740
	481	ТĞ	GTT	CTT	'GG'I	rcc?	\GT(CGG	ACT	3GA(CGG	ACCA	AGTI	TCC	GAA	GAT	AGG	GTC	GCT	GTA	GCGG	* ·
a		T	K	N	Q	v	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	-
	<u>.</u>		'GGA	GTG	:GG/	AGA	GCA.	ATG	GGC	AGC	CGGI	AGA/	ACAZ	CTA	CAA	GAC	CAC	GCC	TCC	CGT	GCTG	600
	541	CA	CCI	CAC	CC	rct	CGT'	TAC	CCG'	TCG	GCC'	rcT	rgti	rg a n	rgŤi	CTC	GTG	SCGG	AGG	IGCA	CGAC	
a		V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	Ţ	T	P	P	V	L	-

FIG. 22B

	C O 1	GA	CTC	CGA	CGG	CTC	CTT														+	660
	601	CT	GAG	GCT	GCC	GAG	GAA	•													CGTC	
		D	s	D	G	S	F	F	L	Y	S	K	L	T	v	D	K	S	R	W	Q	•
·	661				-+-			+				+	• • •		-+-			+	• • •		GCAG + CGTC	720
		Q	G	N	v	F	s	С	s	v	M	Н	E	A	L	Н	N	Н	Y	T	Q	-
											Ва	mHI i	,									
	721				CTC -+- GAG							+			757	•						
		734	C	+	c	T.	C	ъ	G	ĸ	*											

FIG. 23A

	140	I TAT																				
	1				- + -			+ -							. +		• •	-+-		GGA	+	60
		GTA	\TA(CCT	GTT'	rtga	4GTC	31'G'1	YACA	_							I GAC	_		CCT		
3			M	D	K	T	H	T	С	P	P	С	P	A	P	E	L	L	G	G	P	•
	61							CCC#				GGA (CACC	CTC	CAT(AT(CTCC	CGG	SACC	CCT	GAG	120
	4		rca?	AAA(GGA	GAA	GGG	3GG1	r T TI	rgg(STTC	CCT	GTGC	GAG	ATE	CTAC	JAGO	GCC	TGG	GGA	CTC	
a		S	V	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P	E .	•
	404																				TAC	180
	121.																				ATG	100
a		v	T	С	V	v	v	D	v	s	Н	E	D	P	E	v	K	F	N	W	Y	-
		GT(iga(CGG	CGT	GGA	GGT	GCAT	raaj	rgCo	CAAC	GAC	AAA (3CCC	GCGC	GA (GA C	3CA(TAC	AAC	AGC	
	181	• •			-+-			+-		• • •		+			-+			+-			TCG	240
																			•		S	_
3		V	D	G	V	E	V	Н					K			E	E	Q	Y	N		•
	241				-+-			+ -				+ •			+- •		• • • •	+ -	• • • •			300
		TG	CAT	GGC	ACA	CCA	GTC	GCA (GA C	TG(SCA (GGA (CGT	GTC	CTC	SAC	CGAC	CTT?	ACCG	TTC	CTC	
a		T	Y	R	V	V	S	V	L	T	V	L	Н	Q	α	W	L	N·	G	K	E	~
	201																			TCC	AAA +	360
	301	ATO	GTT(CAC	GTT	CCA		•													TTT	
a		Y	ĸ	С	K	v	s	N	K	A	L	P	A	P	I	E	K	T	I	S	K	•
		GC	CAA	AGG	GCA	GCC	CCG	AGA <i>I</i>	ACCA	CAC	GT(GTA(CAC	CTC	JCC (CCC	ATCO	CCGC	GAI	GAG	CTG	400
	361	CG	 GTT'	rcc	- + - CGT	CGG	GGC:	+ · rcti	rgg1	rgt(CCA	+ · CAT(GTG	GAC	CGGC	GG:	rago	GCC	CTA	CTC	GAC	420
a		Α	ĸ	G	0	P	R	E	P			Y		L	P	P	s	R	D		L	-
-				CAA	CCA	ርርጥ የ	CAGO	ርርጥ(FACO	TTGO	CTC	GGT	CAA	\GG(CTTC	CTA!	rcco	CAGO	CGAC	ATC	GCC	
	421				-+-			+				+			- + - •		• • • •	+				480
a																	P			I		•
	481				-+-			+				+			-+-		w - '-	· - + ·	~~ ~ .		CTG	540
	101	CA	CCT	CAC	CCT	CTC	GTT.	ACC	CGT	CGG	CCT	CTT(GTT(GAT(GTT(CTG	GTG	CGG	AGGC	CAC	GAC	
a		v	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T	P	P	V	L	-
	_	GA	CTC	CGA	CGG	CTC	CTT	CTT	CCT	CTA	CAG	CAA	GCT	CAC	CGT	GGA(CAA	GAG	CAGO	TGG	CAG	600
	541	CT	GAG	GCT	- + - GCC	GAG	GAA	+ GAA	GGA(GAT(GTC	GTT	CGA	GTG	GCA	CCT	GTT	CTC	GTC	CACC	GTC	VVV
a		D	S	D	G	S	F	F	L	Y	S	K	L	T	v	D	K	s	R	W	Q	•

FIG. 23B

	C 0 1	CA	GGG	GAA	CGT	CTT	CTC	ATG	CIC	CGA	GAI	+	TGA 		.TCI	GCA	CAA 	4	· · · ·		- + - +	660
	601	GT	ccc		•																CGTC	
a		Q	G	N	V	F	S	C	S	٧	M	Н	E	A	L	Н	N	Н	Y	T	Q	•
	661		. n n		- + -	• • •		+			.	+		• • •	-+-			+			TGAC + ACTG	720
a		K											G								D	-
																	amH	1				
	721				-+-			+			- -	+	ACG		-+-			+		77	3	
a		Ţ	н	v	М	W	E	W	E	C	F	E	R	L	*							

FIG. 24A

	N	Ndeļ .	
	1	CATATGGTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTTGAACGT)
		GTATACCAACTTGGCTTGACACTGTAGGTACAATACACCCTTACCCTTACAAAACTTGCA	
a		MVEPNCDIHVMWEWECFER-	
	61	CTGGGTGGTGGTGGTGACAAAACTCACACATGTCCACCGTGCCCAGCACCTGAACTC	0
		GACCCACCACCACCACTGTTTTGAGTGTACAGGTGGCACGGGTCGTGGACTTGAG	
a		L G G G G D K T H T C P P C P A P E L -	
	1 7 1	CTGGGGGGACCGTCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC	
	121	GACCCCCTGGCAGTCAAAAGGAGAAGGGGGGTTTTTGGGTTCCTGTGGGAGTACTAGAGG	U
a		L G G P S V F L F P P K P K D T L M I S	
		CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG	
	181	GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC	0
a		RTPEVTCVVVDVSHEDPEVK -	
u		TTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG	
	241		0
		AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCCTCCTC	
a		FNWYVDGVEVHNAKTKPREE -	
		CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG	
	301		0
a		QYNSTYRVVSVLTVLHQDWL-	
	361	AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA	0
		TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT	
a		NGKEYKCKVSNKALPAPIEK -	
	401	ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC	Ω
	421	TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGG	U
a		TISKAKGQPREPQVYTLPPS	
		CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG	
	481	GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGAC	0
a		R D E L T K N Q V S L T C L V K G F Y P -	
		AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG	
	541		0
a		SDIAVEWESNGQPENNYKTT -	
·		SUBSTITUTE SHEET (RULE 26)	

FIG. 24B

	601			* * *	-+-			+				+			-+-			+			GTTC	660
a		P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	· L	T	v	D	K	-
	661				-+-	• • •		+		• • •		+			-+-	• • •		+			CAAC + GTTG	720
a		S	R	W	Q	Q	G	N	V	F	S	С	S	v	M	Н	E	A	L	Н	N	•
																B	amH	I				
	721				GCA -+- CGT			+				+		.	-+-			+		77	3	
a		н	V	ďΓ	0	K	S	Ţ,	S	L	S	P	G	K	*							

FIG. 25A

No	leI 																				
1	CAT	TAT	GA(CAA) - + -	AAC'	TCA	CAC +	ATG	TCC	ACC	TTG +	TCC	AGC	TCC -+-	GGA.	ACT	CCT(GGG	GGG	ACCG	60
	GTA	ATA	CCT	GTT'	TTG	AGT	gtg	TAC	AGG	TGG	AAC	AGG	TCG	AGG	CCT'	TGA	GGA	CCC	CCC	rggc	
		M	D	K	T	H	T	C	P	P	C	P	A	P	E	L	L	G	G	P	-
61	TCA	AGT	CTT	CCT(CTT	CCC	CCC +	AAA 	ACC	CAA	GGA +	CAC	CCT	CAT	GAT	CTC	CCG	GAC	ccc'		120
	AGT	CAC	GAA(3GA	GAA	GGG	GGG	TTT	TGG	GTT	CCT	GTG	GGA	GTA	CTA	GAG	GGC	CTG	GGG	ACTC	
	S	V	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P	E	•
121	GTC	CAC	ATG	CGT(GGT	GGT	GGA	CGT	GAG	CCA	CGA +	AGA	CCC	TGA	GGT	CAA	GTT(CAA	CTG		180
12.1	CAC	STG	rac	GCA(CCA	CCA	CCT	GCA	CTC	GGT	GCT	TCT	GGG	ACT	CCA	GTT	CAA	GTT	GAC	CATG	
	v	T	C	V	v	V	D	V	S	Н	E	D	P	E	V	K	F	N	W	Y	-
101	GTO	3GA(CGG	CGT(GGA(GGT	GCA	TAA	TGC	CAA	GAC	AAA	GCC	GCG	GGA	ĠGA(GCA	GTA	CAA		240
181	CAC	CT	GCC	GCA	CCT	CCA	CGT	ATT	ACG	GTT	CTG	TTT	CGG	CGC	CCT	CCT	CGT	CAT	ĠTT		2.40
	v	D	G	v	E	v	Н	N	A	K	T	ĸ	P	R	E	E	Q	Y	N	S	-
	ACC	TA(CG'	rgt	GGT	CAG	CGT	CCT	CAC	CGT	CCT	GCA	CCA	GGA	CTG	GCT	GAA'	TGG	CAA	GGAG	300
241	TGC	CAT	GGC	-+- ACA	CCA	GTC	GCA	GGA													300
	T	Y	R	V	v	S	v	L	T	v	L	Н	Q	D	· W	L	N	G	K	E	•
																	AAC	CAT	CTC		260
301	ATO	GTT(CAC	- + - GTT	CCA	GAG	GTT	GTT	TCG	GGA	GGG	TCG	GGG	GTA	GCT	CTT	TTG	GTA(GAG		360
	Y	K	C	K	v	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	-
	GC	CAA	AGG	GCA	GCC																420
361	CG	 3TT'	rcc	-+- CGT	CGG																420
	A	K	G	Q	P	R	E	P	Q	V	Y	T	L	P	P	s	R	D	E	L	-
	ACC	CAA	GAA	CCA	GGT	CAG	CCT	GAC	CTG	CCT	GGT	CAA	AGG	CTT	CTA	TCC	CAG	CGA	CAT	CGCC	400
421	TG	 3TT(CTT	- + - GGT	CCA	GTC	+ GGA	CTG	GAC	GGA	CCA	GTT	TCC	GAA	GAT.	AGG	GTC	GCT	GTA	GCGG	400
	T	K	N	Q	v	S	L	T	C	L	v	K	G	F	Y	P	s	D	I	A	•
	GT	GGA(GTG(GGA	GAG	CAA	TGG	GCA	.GCC	GGA	.GAA	CAA	CTA	CAA	GAC	CAC	GCC	TCC	CGT	GCTG	
481	- 41.			-+-			+			•	+			-+-		,	+			+	540
																					•
	GAG	ርጥር	CGA	CGG	CTC	CTT	СТТ	CCT	ста	.CAG	CAA	.GCT	CAC	CGT	GGA	CAA	GAG	CAG	GTG	GCAG	
541				- + -			+				+			-+-			+		• • •	+	600
	~ . '	× ·· · ·									K										
	1 61 121 181 301 361 421	1 GTA 1 GTA 61 AGA 8 GTA 121 CAC V 181 CAC V 241 TGC T 301 ATC Y 361 CGC A 421 TGC T 481 CAC V GAC GAC	CATATO GTATAO M TCAGTO AGTCAO S V 121 CAGTO V T GTGGAO T Y TACAAO Y K GCCAA ATGTTO Y K 361 CGGTT A K 421 TGGTT T K 481 CACCT V E GACTO V E GACTO	CATATGGAG GTATACCTG M D TCAGTCTTG AGTCAGAAG S V F CAGTGTACG V T C GTGGACGGG V D G ACGTACCGG T Y R TACAAGTGG Y K C GCCAAAGGG ATGTTCACG Y K C GCCAAAGGG A K G ACCAAGAAG ACCAAGAAG T K N GTGGAGTG T K N GACTCCGA T CACCTCACG T CACCTCAC	CATATGGACAA GTATACCTGTT M D K TCAGTCTTCCT AGTCAGAAGGA S V F L GTCACATGCGT CAGTGTACGCA V T C V GTGGACGGCGT CACCTGCCGCA V D G V ACGTACCGTGT T Y R V TACAAGTGCAA T Y R V TACAAGTGCAA ATGTTCACGTT Y K C K GCCAAAGGGCA A K G Q ACCAAGAACCA T GGTTCCCGT A K G Q ACCAAGAACCA T GGTTCTTGGT T K N Q GTGGAGTGGGA 421 TGGTTCTTGGT T K N Q GTGGAGTGGGA 481 CACCTCACCCT V E W E GACTCCGACGG	CATATGGACAAAAC GTATACCTGTTTTG M D K T TCAGTCTTCCTCTTC AGTCAGAAGGAGAA S V F L F GTCACATGCGTGGT CAGTGTACGCACCA V T C V V GTGGACGGCGTGGAA CACCTGCCGCACCT V D G V E ACGTACCGTGTGGT T Y R V V TACAAGTGCAAGGT T Y R V V TACAAGTGCAAGGT Y K C K V GCCAAAGGGCAGCC A K G Q P ACCAAGAACCAGGT TGGTTCTTGGTCCA T K N Q V GTGGAGTGGGAGAG CACCTCACCCTCTC V E W E S GACTCCGACGGCTCC	CATATGGACAAAACTCA GTATACCTGTTTTGAGT M D K T H TCAGTCTTCCTCTTCCC AGTCAGAAGGAGAAGGG S V F L F P GTCACATGCGTGGTGGT CAGTGTACGCACCACCA V T C V V V STGGACGGCGTGGAGGT TGCATGCCGCACCTCCA V D G V E V ACGTACCGTGTGGTCAG TY R V V S TACAAGTGCAAGGTCTC TY R V V S TACAAGTGCAAGGTCTC ATGTTCACGTTCCAGAG Y K C K V S GCCAAAGGGCAGCCCCG A K G Q P R ACCAAGAACCAGGTCAG TGGTTTCCCGTCGGGGC T K N Q V S GTGGAGTGGGAGAGCAA 481 CACCTCACCCTCTCGTT V E W E S N GACTCCGACGGCTCCTT	CATATGGACAAAACTCACAC GTATACCTGTTTTGAGTGTG M D K T H T TCAGTCTTCCTCTTCCCCCC AGTCAGAAGGAGAAGGGGGG S V F L F P P GTCACATGCGTGGTGGTGGAG CAGTGTACGCACCACCACCT V T C V V V D GTGGACGGCGTGGAGGTGCA CACCTGCCGCACCTCCACGT V D G V E V H ACGTACCGTGTGGTCAGCGT T Y R V V S V TACAAGTGCAAGGTCTCCAA T Y R V V S V ATGTTCACGTTCCAGAGGTT Y K C K V S N GCCAAAGGGCAGCCCCGAGA ATGTTCCCGTCGGGGCTCT A K G Q P R E ACCAAGAACCAGGTCAGCCT T GGTTCTTGGTCCAGTCGGA T K N Q V S L GTGGAGTGGGAGAGCAATGG T K N Q V S L GTGGAGTGGGAGAGCAATGG T K N Q V S L GTGGAGTGGGAGAGCAATGG CACCTCACCCTCTCGTTACC V E W E S N G GACTCCGACGGCTCCTTCTT	CATATGGACAAAACTCACACATG GTATACCTGTTTTGAGTGTGTAC M D K T H T C TCAGTCTTCCTCTTCCCCCCAAA AGTCAGAAGGAGAAGGGGGGTTT S V F L F P P K GTCACATGCGTGGTGGTGGACGT CAGTGTACGCACCACCACCTGCA V T C V V V D V GTGGACGGCGTGGAGGTGCATAA CACCTGCCGCACCTCCACGTATT V D G V E V H N ACGTACCGTGTGGTCAGCGTCCT TGCATGGCACACCACCACCTCCACGTATT Y R V V S V L TACAAGTGCAAGGTCTCCAACAA ATGTTCACGTTCCAGAGGTTGTT Y K C K V S N K GCCAAAGGGCAGCCCCGAGAACC A K G Q P R E P ACCAAGAACCAGGTCAGCCTTGG A K G Q P R E P ACCAAGAACCAGGTCAGCCTGAC T K N Q V S L T GTGGAGTGGGAGACCAGCCTGACCACAA 481 CACCTCACCCTCTCGTTACCCGT V E W E S N G Q GACTCCGACGGCTCCTTCTTCCT	CATATGGACAAAACTCACACATGTCC GTATACCTGTTTTGAGTGTGTACAGG M D K T H T C P TCAGTCTTCCTCTTCCCCCCAAAACC AGTCAGAAGGAGAAGGGGGGTTTTGG S V F L F P P K P GTCACATGCGTGGTGGTGGACGTGAG CAGTGTACGCACCACCACCTGCACTC V T C V V V D V S GTGGACGGCGTGGAGGTGCATAATGC CACCTGCCGCACCTCCACGTATTACG V D G V E V H N A ACGTACCGTGTGGTCGAGCGTCCTCAC T Y R V V S V L T TACAAGTGCAAGACCAGCTGCACGAGAGTG T Y R V V S V L T TACAAGTGCAAGGTCTCCAACAAAGC ATGTTCACGTTCCAGAGGTTGTTCG Y K C K V S N K A GCCAAAGGGCAGCCCCGAGAACCACA 361 GGCTTTCCCGTCGGGGCTCTTGGTGT A K G Q P R E P Q ACCAAGAACCAGGTCAGCCTGACCTG T K N Q V S L T C GTGGAGTGGGAGAGCAATGGGCAGCC 481 CACCTCACCCTCTCTTACCCGTCGGG V E W E S N G Q P GACTCCGACGGCTCCTTACTTACCTTA	CATATGGACAAAACTCACACATGTCCACC GTATACCTGTTTTTGAGTGTGTACAGGTGG M D K T H T C P P TCAGTCTTCCTCTTCCCCCCAAAACCCAA AGTCAGAAGGAGAAGGGGGGTTTTGGGTT S V F L F P P K P K GTCACATGCGTGGTGGTGGACGTGAGCCA CAGTGTACGCACCACCACCTGCACTCGGT V T C V V V D V S H GTGGACGGCGTGGAGGTGATTACGGTT V D G V E V H N A K ACGTACCGTGTGGTCACACCACCTCACCGT TGCATGGCACACCACCACCTCCACGTATTACGGTT V D G V E V H N A K ACGTACCGTGTGGTCAGCGTCCTCACCGT TY R V V S V L T V TACAAGTGCAAGGTCTCCAACAAAGCCCT ATGTTCACGTTCCAGAGGTTGTTTCGGGA Y K C K V S N K A L GCCAAAGGGCAGCCCCGAGAACCACAGGT CGGTTTCCCGTCGGGGCTCTTGGTGTCCA A K G Q P R E P Q V ACCAAGAACCAGGTCAGCCTGACCTGCCT TGGTTCTTGGTCCAGTCGGACTGGACGGA T K N Q V S L T C L GTGGAGTGGGAGAGCCATGCCCGA 481 CACCTCACCCTCTCGTTACCCGTCGGCCT V E W E S N G Q P E GACTCCGACGGGCTCCTTCCTTCCTCACAG	CATATGGACAAAACTCACACATGTCCACCTTG GTATACCTGTTTTGAGTGTGTACAGGTGGAAC M D K T H T C P P C TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGA AGTCAGAAGGAGAGGGGGGTTTTGGGTTCCT S V F L F P P K P K D GTCACATGCGTGGTGGTGGACCTCGGTGCT V T C V V V D V S H E GTGGACGGCGTGGAGGTGAATATGCCAAGAC CACCTGCCGCACCTCCACGTATTACGGTTCTG V D G V E V H N A K T ACGTACCGTGTGGTCAGCGTCCTCACCGTCCT TGCATGGCACACCAGGTCGCAGGAGGAGGAGAACCACGGAGAA T Y R V V S V L T V L TACAAGTGCAAGGTCTCCAACAAAGCCCTCCC ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGG Y K C K V S N K A L P GCCAAAGGGCAGCCCCGAGAACCACAGGTGTA A K G Q P R E P Q V Y ACCAAGAACCAGGTCAGCCTGGACCTGCTGGT TGGTTCTTGGTCCAGTCGGACCTGCCTGGT T K N Q V S L T C L V GTGGAGTGGGAGAGCAAATGGCCGGACCAC T K N Q V S L T C L V GTGGAGTGGGAGAGCAAATGGCCGGACCACAGAAA CACCTCACCCTTCTCTTACCCGTCGGCCTCTT V E W E S N G Q P E N GACTCCGACGGCTCCTCTTCCTCACAGCAA	CATATGGACAAAACTCACACATGTCCACCTTGTCC CATATGGACAAAACTCACACATGTCCACCTTGTCC GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGG M D K T H T C P P C P TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTG S V F L F P P K P K D T GTCACATGCGTGGTGGTGGACGTGACCACCACAAGACAACAAA 121 CAGTGTACGCACCACCACCACCTGCACTGGGTGCTTCT V T C V V V D V S H E D GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA 181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTT V D G V E V H N A K T K ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCA T Y R V V S V L T V L H TACAAGTGCAAGGTCTCCAACAAAAGCCCTCCCAGG Y K C K V S N K A L P A GCCAAAAGGGCAGCCCCGAGAACCACAGGTGTACACA 361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACCATGTG A K G Q P R E P Q V Y T ACCAAGAACCAGGTCAGCCTGGACCTGCCTGGTCAACAAGACCAAGGTTCCAACAAGGCCTCCACCATGTG T K N Q V S L T C L V K GTGGAGTGGGAAGCAACAACAACAACAACAACAAAACCCAGGTTTCAACAACAAAACCAAGGTCCTCCAACAAAACCAAGGTCTCAACAACAAAACCCAGGTTCCAACAACAACAACAACAACAACAACAACAACAACAAC	CATATGGACAAAACTCACACATGTCCACCTTGTCCAGC GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCG M D K T H T C P P C P A TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGA S V F L F P P K P K D T L GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCC CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGG V T C V V V D V S H E D P GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC 181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGG V D G V E V H N A K T K P ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCA T Y R V V S V L T V L H Q TACAAGTGCAAGGTCTCCAACAAAAGCCCTCCCAGGCCCC Y K C K V S N K A L P A P GCCAAAAGGCCAGCCCGAGAACCACAGGTGTACACCCT ATGTTCCCGTCGGGGGCTCTTGGTGTCCACATGTGGGA A K G Q P R E P Q V Y T L ACCAAGAACCAGGTCAGCCTGGACCTGCCTGGACCACATGTGGGA A K G Q P R E P Q V Y T L ACCAAGAACCAGGTCAGCCTGGACCTGCCTGGTCAAAAGG T K N Q V S L T C L V K G GTGGAGTGGGAGAGCAAATGGGCAGCCGGAGAACAACTA 481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGAT V E W E S N G Q P E N N Y GACTCCGACGGCTCCTTCTTCTCACAGCAAGCTCACA	CATATGGACAAACTCACACATGTCCACCTTGTCCAGCTCC GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGG M D K T H T C P P C P A P TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTA S V F L F P P K P K D T L M GTCACATGCGTGGTGGTGGACCTGGACCCACGAAGACCCTGAT CAGTGTACGCACCACCACCTGCACTCGGTGGTTCTGGGACT V T C V V V D V S H E D P E GTGGACGGCGTGGAGGTCCTAAATGCCAAGAACAAAGCCGCG V D G V E V H N A K T K P R ACGTACCGTGTGGTCACCGTCCTCACCGTCCTGCACCAGGA ACGTACCGTGTGGTCCACCGTCCTCACCGTCCTGCACCAGGA T Y R V V S V L T V L H Q D TACAAGTGCAAGGAGGTCTCCAACAAAGCCCTCCAGGCCCCAT Y K C K V S N K A L P A P I GCCAAAGGGCACCCCGAGGAACCACAGGTGTACACCCTGCC A K G Q P R E P Q V Y T L P ACCAAGAACCAGGTCAGCCTGGACCTGCCTGCACCAGGA 421 TGGTTCTTGGTCCAGTCGAGCTTGGACTGCCTGACCCTGCC A K G Q P R E P Q V Y T L P ACCAAGAACCAGGTCAGCCTGACCTGCCTGCACCATGTGGGACGG A K G Q P R E P Q V Y T L P ACCAAGAACCAGGTCAGCCTGACCTGCCTGCACAAAGGCCTTCCAAAAGCCTTCCCAACAAACCACAGGTGTACACCCTGCC T K N Q V S L T C L V K G F GTGGAGTGGGAGAGCAATGGGCAGCCCGGAGAACAACTACAAA 481 CACCTCACCCTCTCGTTACCCGTCGGCCCCTTTGTTGATGTTT V E W E S N G Q P E N N Y K GACTCCGACGGCTCCTTCTTCTCTCTACAGCAAGCTCACCCTGCTCACCCTTCTTTTTTTT	CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGA. GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCT M D K T H T C P P C P A P E TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGAT. AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTA. S V F L F P P K P K D T L M I GTCACATGCGTGGTGGTGGACCTCGGTGCTTCTGGGACTCCA. V T C V V V D V S H E D P E V GTGGACGGCGTGGAGGTGACCACAGAAAAGCCCTGAGAT. CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGGGCCCT. V D G V E V H N A K T K P R E ACGTACCGTGTGGTCAGCGAGGAGGACGTGGTCCTGACCAGGACTGACCAGACAAAGCCGCGGGA. T Y R V V S V L T V L H Q D W TACAAGTGCAAGGTCTCCAACAAAAGCCCTCCAGGCCCCATCGA. 301 ATGTTCACGTTCCAGAGGTTGTTTTCGGGAGGGTGGCTGGGGTAGCT. Y K C K V S N K A L P A P I E GCCAAAAGGCCAGCCGGAGAACCACAGGTGTACACCCTGCCCC. 361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGAACAAAGCCCTGCCCCCCCC	CATATGGACAAAACTCACACATGTCCACCTTGTCCAGGTCGGAACT GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGA M D K T H T C P P C P A P E L TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAG S V F L F P P K P K D T L M I S GTCACATGCGTGGTGGTGGACCACCTGCACTGGTCTTCTGGGACTACTAGAG V T C V V V D V S H E D P E V K GTGGACGGCGTGGAGGTCATAATGCCAAGACAAAGCCCTGAGGTCAA 181 CACCTGCCGCACCTCCACGTTATTACGGTTCTGTTTCGGCGCCCTCCT V D G V E V H N A K T K P R E E ACGTACCGTGTGTGAGCACACGTCCTCCTGCACCAGGACTGCCTCTT TGCATGGCAACACCAGTCCAAGAAGACCACAGGACTGGCT T Y R V V S V L T V L H Q D W L TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAA 301 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGTCGGGGTAGCTCT Y K C K V S N K A L P A P I E K GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCATGCCCCCATC A K G Q P R B P Q V Y T L P P S ACCAAGAACCAGGTCAGCCTGGACCTGGCCTGAACAAGGCTTCTATCC 421 TGGTTCTTGGTCCAGTCGGACTTGGTGCACAAAAGGCTTCCAACAAGACCAGGTTACACCATGCCCCCATC A K G Q P R B P Q V Y T L P P S ACCAAGAACCAGGTCAGCCTGACCTGGCCTGGACAAAAGGCTTCTATCC 421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGGTTTCCGAAGATAGG T K N Q V S L T C L V K G F Y P GTGGAGTGGGAAGACAATGGGCAGCCGGAGAACAACTACAAGACCAC 481 CACCTCACCCTCTCTGTTACCCGTCGGCCTCTTGTTGATGTTCTGTTG V E W E S N G Q P E N N Y K T T GACTCCGACGGCTCTTTCTTCCTTACAGAAAGCTCACCCTTGGACAA	CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCT GTATACCTGTTTTGAGTGTGTACAGGTGAACAGGTCGAGGCCTTGAGGA M D K T H T C P P C P A P E L L TCAGTCTTCCTCTTCCCCCCAAAACCCAAGACACCCTCATGATCTCCCG AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGC S V F L F P P K P K D T L M I S R GTCACATGCGTGGTGGTGGACCTCGGTGCTTCTGGGACTCCAGTTCAA V T C V V V D V S H E D P E V K F GTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAC 181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCTCTGTV V D G V E V H N A K T K P R E E Q ACGTACCGTGTGTGTCACGGTCCTCACCGTCTGGACCAGGACTGGCTGAAC T Y R V V S V L T V L H Q D W L N TACAAGTGCAAGGTTCCAACAAAGCCCTCCAGCGCCCCATCCAGAAAAAC 301 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGTCGGGGGTAGCTTTTG Y K C K V S N K A L P A P I E K T GCCAAAGGGCAGCCCCGAGAACCAACAGGTGTTCCACCGTCCCGGAGAAAAC 361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCT T K N Q V S L T C L V K G F Y P S GTGGAGTGGGAGAGCAATGGCCAGCCCCCAAGAACAAACCACGCCC T K N Q V S L T C L V K G F Y P S GTGGAGTGGGAGAGCAATGGCCAGCCCCCAAGAACAACACACAGCCCCCCAACAAACCACC	CATATGGACAAACTCACACATGTCCACCTTGTCCAGGCTCGGAACTCCTGGGA GTATACCTGTTTTGAGTGTGTACAGGTGAACAGGTCGAGGCCTTGAGGACCCC M D K T H T C P P C P A P E L L G TCAGTCTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCAAAACCCAAGAACCCCTCATGATCTCCCCGGACCCCAAAACCCAAGAACCCCTCATGATCTCCCCGGACCCCCAAAACCCCAAGAACCCCTCATGATCTCCCCGGACCCCCAAAACCCAAGACCCCTCATGATCTCCCCGGACCCCCAAAACCCAAGACCCCTCATGATCTCACGAGGCCTGAGGTCAAGTTCAACCCCACCACCACCACCACCACCACCACCACCACCA	CARATGGACAAAACTCACACATGTCCACCTTGTCCAGGCTCGGAACTCCTGGGGGG GTATACCTGTTTTGAGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCC M D K T H T C P P C P A P E L L G G TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCGGGACCCCC AGTCAGAAGGAGAAGGGGGGTTTTGGTTCCTGTGGAGTACTAGAGGGCCTGGGG S V F L F P P K P K D T L M I S R T P GTCACATGCGTGGTGGACCCTGCACTGGTGTCTTGGGAGTCCAGGTTCAAGTTCAACTGG V T C V V V D V S H E D P E V K F N W GTGGACGGCGTGGAGGTCATAATGCCAAGACAAAGCCCGCGGGAGGACACTACAAGTTCAACTGG 181 CACCTGCCGCACCTCCACGTATTACGGTTCTTTTTGGGGGCCCTCCTCGTCATGTTC V D G V E V H N A K T K P R E E Q Y N ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAC 241 TCCATGCCACCACCAGTCGAGGAGTGGAGGAGGAGGACACAGGCTGAACTGCTTC T Y R V V S V L T V L H Q D W L N G K TACAAGTGCAAGAGGTCTCCAACAAAGCCCTCCAGGCGGGGAAAAACCACTCTC A K G Q P R E P Q V Y T L P P S R D E ACCAAGAACCAGGTCAGCCTGGACCTGGCACAAAAGGCCTCCCAGGGAAGAACCACTGTCACACTTACCGTTC A K G Q P R E P Q V Y T L P P S R D E ACCAAGAACCAGGTCAGCCTGACCTGCACCAGGACTAGGGGGGAAGAACCACTGTCACCGTTCACCGTTCACCGTTCACCGTTCACCGTTCACCGTCACCAGGACTACCCGGGACACACAC	CTATATGGACAAAACTCACACATGTCCACCTTGTCCAGGTCGGAACTCCTGGGGGGACCG GTATACCTGTTTTGAGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC M D K T H T C P P C P A P E L L G G P TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCCGGACCCCTGAG AGTCAGAAGGAGAAGGGGGTTTTGGGTTCCTGTGGGACTCCTGGGACCCCTGAG S V F L F P P K P K D T L M I S R T P E GTCACATGCGTGGTGGTGGACCTCGGTGCTTCTGGGACTCCAGTTCAAGTTCAACTGGTAC 121 CAGTGTACCGACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTCAACTGGTAC V T C V V V D V S H E D P E V K F N W Y GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCTGGGGAGGAGAGAGA

FIG. 25B

a		F	T	L	C	*																
	721				-+-	CTA		GAT		CTCG SAGO		748	3									
A		K	S	L	S	L	S	P	G	K.	G	G	G	G	G	C	Т	T	H	W	G	•
	661				- 4 -			+				+			-+-			+			GGGT + CCCA	120
a		Q	G	N	V	F	S	C	S	V	M	Н	E	A	L	Н	N	H	Y	T	Q	•
	601							+				+			-+-			+			GCAG + CGTC	660

FIG. 26A

	Nd	eI																			
	_	CATAI	GTG	CAC	CAC	CCA	CTG	GGG:	rtt	CAC	CCT	GTG(CGGI	rgg <i>i</i>	\GGC	GG	rgg(GAC	CAAP	AGGT	60
	1	GTATA	CAC	GTG	GTG	GGT	GAC	CCC	AAA	GTG(GGA	CAC	GCC <i>I</i>	ACCI	CCC	SCC?	ACC	CCTO	TTT	CCA	
a		М	С	T	T	Н	W	G	F	T	L	C	G	G	G	G	G	D	K	G	-
		GGAGG	CGG	TGG	GGA	CAA	AAC	TCA	CAC	ATG'	rcc	ACC!	rtgo	CCCA	AGC?	ACC	rga/	ACTO	CTC	SGGG	120
	61	CCTC	CGCC	ACC	CCT	GTT	TTG	AGT(GTG:	rac:	AGG'	rggi	AAC	GG7	rCGI	rggi	ACT	rgac	GAC	cccc	
a		G G	G	G	ם	ĸ	T	н	T	С	P	P	С	P	A	P	E	L	L	G	•
		GGAC	CGTC	AGT	TTT	CCT	CTT	CCC	CCC	AAA	ACC	CAA	GGA	CAC	CTC	CAT	GAT(CTC	CCG	SACC	180
	121	CCTG	GCAG	TCA	AAA	GGA	GAA	GGG	GGG'	TTT'	TGG	GTT	CCT	STGO	GA (GTA(CTA	GAG	GGC(CTGG	
a		G P	S	v	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	-
		CCTG	AGGI	CAC	ATG	CGT	GGT	GGT	GGA	CGT	GAG	CCA	CGA	AGA(ccc'	rga(GGT	CAA	GTT(CAAC	240
	181	GGAC'	TCCA	GTG	TAC	GCA	CCA	CCA	CCT							ACT	CCA	GTT(CAA	GTTG	
a		P E	V	T	С	v	V	V	D	V	S	Н	E	D	P	E	V	K	F	N	•
		TGGT	ACGI	rgga	\CGG	CGI	GGA	GGT	GCA	TAA	TGC	CAA	GAC.	AAA	GCC	GCG	GGA	GGA	GCA(GTAC	300
	241	ACCA	TGC.	· - + -	GCC	CGCA	CCI	CCA	CGT	ATT	ACG	GTT	CTG	TTT	CGG	CGC	CCT	CCT	CGT		300
a		W Y	v	D	G	V	E	v	H	N	A	K	T	K	P	R	E	E	Q	Y	-
		AACA	GCAC	CGTA	ACCO	TGI				CCT	CAC	CGT	CCT	GCA	CCA	GGA	CTG	GCT	GAA'	TGGC	360
	301	TTGT	CGT	CAT	rgg(CACA		GTC		.GGA	GTG	GCA	.GGA	CGT	GGT	CCT	GAC	CGA	CTT.		
a		n s	T	Y	R	V	v	S	V	L	T	V	L	Н	Q	D	W	L	N	G	•
		AAGG	AGT?	ACAI	AGT	GCA!	AGGI	CTC	CAA	CAA	AGC	CCT	ccc	AGC	CCC	CAT	CGA	GAA	AAC	CATC	420
	361	TTCC	TCA	rgr	rca(CGT	rcc?	GAG	GTT	GTT						GTA	GCT	CTT	TTG	GTAG	
a		K E	Y	K	C	ĸ	V	s	N	K	· A	L	P	A	P	I	E	K	T	I	•
		TCCA	AAG	CCA	AAG (GGC1	AGC	CCC	AGA	ACC	ACA	GGI	GTA	CAC	CCT	GCC	CCC	ATC	CCG	GGAT	480
	421	AGGT	TTC	GGT:	rtc(CCG	rcgo	SGGC	TCI	TGC	TGI	CCA	CAT	'GTG	GGA	CGG	GGG	TAG	GGC	CCTA	
a		s K	A	K	G	Q	P	R	E	P	Q	٧	Y	Ţ	L	P	P	S	R	D	•
		GAGO	TGA	CCA	AGA	ACC	AGG:	rca(CCI	GAC	CTO	CCI	GGT	CAA	AGG	CTI	CTA	TCC	CAG	CGAC	540
	481	CTCG	ACT	GGT	rct'	TGG	rcci	AGTO	CGGA	CTO	GAC	CGGA	CCA	GTI	TCC	GAA	GAT	'AGG	GTC	GCTG	•
a		E L	т	K	N	Q	v	s	L	T	C	L	v	K	G	F	Y	P	S	D	-
		ATC	CCG	TGG	AGT	GGG:	AGA(GCA?	ATGO	GC <i>I</i>	AGC	CGG?	\GAA	CAA	CTA	CAA	AGAC	CAC	GCC	TCCC	600
	541	TAGO	CGGC	ACC'	TCA	CCC	TCT	CGT	rac(CCG	rcg	3CC7	rcti	rgti	GAT	'GT'I	CTC	GTG	CGG	AGGG	
a		I Z	4 V	E	W	E	s	N	G	Q	Þ	E	N	N	Y	K	T	T	P	P	-

FIG. 26B

	601				-+-			+			*	+			-+-			+		•	CAGG + GTCC	660
a		v	·L	D	S	D	G	S	F	F	L	Y	S	K	L	Т	v	D	K	s	R	•
	661				-+-		• • •	+	~			+			-+-			+			CTAC GATG	
а		W	Q	Q	G	N	V	F	S	C	S	V	M	Н	E	A	L	Н	N	Н	Y	•
	721				-+-		CTC GAG	+				+	ATA	~ ~ ~	GAT		763					
a		T	Q	K	S	L	S	L	S	P	G	K	*									